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July 19, 2006, 06:49:14; Search time 4394 Seconds (without alignments) 10187.345 Million cell updates/sec
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                         US-10-661-966-1_146001-146700_A146311
                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                           6366136 seqs, 31973710525 residues
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Maximum Match 100%
Listing first 70 summaries
                                                    OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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AC006344 Homo sapi AC167793 Bos tauru AC074010 Homo sapi AC07276 Homo sapi AC0255490 Homo sapi AC093671 Homo sapi AC109591 Homo sapi AC109591 Homo sapi AC10869 Pan trogl AC116177 Homo sapi AC116177 Homo sapi AC110584 Homo sapi AC110584 Homo sapi AC110584 Homo sapi AC110596 Homo sapi AC106756 Homo sapi AC106756 Homo sapi AC016756 Homo sapi AC106756 Homo sapi AC016756 Homo sapi AC090150 Homo sapi 5 AC006344 12 AC167793 12 AC07276 12 AC07276 12 AC011079 12 AC109591 12 AC14869 12 AC14869 12 AC14869 12 AC106876 12 AC14669 12 AC161676 5 AC008836 12 AC10684 5 AC008036 12 AC16675 5 AC008022 16.5 159859 16.5 172573 16.5 172573 16.5 169819 16.5 186370 16.5 212421 16.3 156393 16.3 156393 16.1 157492 16.1 191004 16.1 207181 16.1 207181

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8 111 12 12 14 14 15 16 17 18 18

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112.8 112.8 112.8 112.8 112.8

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AC055723 Homo sapi AC062912 Homo sapi AC069048 Homo sapi BV18489 squm14628 BV612024 S217P6184 AC012498 Homo sapi AC092323 Homo sapi AC092323 Homo sapi AC092323 Homo sapi AC053509 Homo sapi AC053509 Homo sapi AC14492 Homo sapi AC055509 Homo sapi AC146076 Pan trogl AC112190 Homo sapi AC112190 Homo sapi AC112190 Homo sapi AC112190 Homo sapi AC010482 Homo sapi	BV639424 \$217P6156 AL67206 Human DNA AC108383 Pan trogsl AC450486 Human DNA AL137842 Homo sapi AC090401 Homo sapi AC09138 Homo sapi AC09138 Homo sapi AC07538 Homo sapi AC07538 Homo sapi AC072055 Homo sapi AC072055 Homo sapi AC072055 Homo sapi AC072055 Homo sapi AC072052 Homo sapi AC072052 Homo sapi AC072052 Homo sapi AC072052 Homo sapi AC01205486 Homo sapi AC012064 Homo sapi AC01206 Homo sapi AC009410 Homo sapi AC07992 Homo sapi AC07992 Homo sapi AC079942 Homo sapi AC079942 Homo sapi	ENTS p DNA linear PRI 21-DEC-1999 N20 from 7q32-q34, complete sequence. Craniata; Vertebrata; Euteleostomi; glires; Primates; Catarrhini; sequence (1998)
ACO5572 PC0929 BV11208 BV11208 BV11208 BV11208 ACO1249 ACO123 ACO9213 ACO9213 ACO9213 ACO9213 ACO9213 ACO9213 ACO9213 ACO9213 ACO9213 ACO1449 ACO1449 ACO1449 ACO1449	BV639424 AL672206 AL672206 AL10838 AC10838 AC10838 AC10834 AC07253 AC07252 AC07252 AC07252 AC072128 AC10797 AC10797 AC108110 AC108110 AC108116 AC108130 AC108116 AC108116 AC108116 AC108116 AC108116	ALIGNM 127447 b ne RP4-726 .50 Chordata; Euarchonto (17) erston, R. uman genome
16.0 166787 16.0 183720 16.0 183720 16.0 186144 16.0 186144 16.1 18.0 18614 16.1 18.0 18323 16.1 18.0 18.0 18.0 16.1 18.0 16.1 18.0 16.1 18.0 16.1 18.0 16.1 18.0	15.7 15.7 15.7 15.6 15.7 15.6 15.7 15.6 15.6 15.6 15.6 15.6 16.6	AC006344 Homo sapiens PAC clon AC006344.2 GI:450811 HOMO sapiens (human) HOMO sapiens Eukaryota; Metazoa; (Bukaryota; Butheria; 1 Hominidae; Homo. 1 (bases I to 12744' I (bases I to 12744' Toward a complete hur Genome Res. 8 (11);
10000000000000000000000000000000000000	00000000 0000 00000000000	RESULT 1 AC006344/c LOCUS DEFINITION ACCESSION VERGION

no read

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                                               The run of A's from 48936 to 48936 may contain one less A, was able to make an exact call.
Location/Qualifiers
1. .127447
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                                                                                                   FEATURES
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov or see http://genome.wustl.edu/gsc
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NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP4-529P3. Actual start of this
clone is at base position 1 of RP4-726N20; actual end is at 127447
                                                                                                                                                                                    Submitted (11-JAN-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 53108, USA 4 (bases 1 to 127447) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (10-701-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 127447)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 24, 1999 this sequence version replaced gi:4139379.
                                                                                                                                                                                                                                                                                                                                               Submitted (24-MAR-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 127447) Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------ Genome Center
Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The clone may be obtained either from Genome Systems, Inc.
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                       2 (bases 1 to 127447)
Cordes,M., Wohldman,P., Pape,K. and Hotic,M.
The sequence of Homo sapiens PAC clone RP4-726N20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: WUGSC
                                                                                                                     3 (bases 1 to 127447)
Waterston, R.H.
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99 121 TARTIGATITIACCAAATITCCATGGAACAACAACGGTTGGCTATTTTTGGATTGGA	Donlin, J., McCauley, S., Dugan-Rocha, S., Dunn, A., Durbin, K., Dziuda, D., Egan, A., Escotto, M., Espinosa, V., Eugene, C., Fa, M., Fernandez, S., Fernando, P., Flagg, N., Forbes, L., Foster, P., Fowler, G., Fu, Q., Fuh, B., Garcia, A., Garcia, R., Garrer, T., Gaskin, C., Gench, S., Ghose, S., Gill, R., Gonzalez, D., Hand, M., Hamilton, K., Harbes, B., Harris, R., Haulak, P., Handi, B., Hamilton, K., Harbes, B., Harris, R., Haulak, P., Hawes, A., Hawkins, B., Hayes, S., Hemphill, L., Herrandez, J., Hawes, A., Hawkins, B., Hayes, S., Hemphill, L., Herrandez, J., Hoobell, L., Jiang, H., Johnson, R., Kalafus, K., Kelly, S., Keys, T., Khan, Z., King, L., Kovar, C., Kowis, A., Kowis, C., Lara, F., Li, Y., Li, Z., Linnell, M., Liu, W., Liu, YS., Liu, Y., Liyanage, D., London, P., Lopez, J., Lorensuhewa, L., Lozado, R., Luk, T., Madu, R., Maheshwari, M., Mahoney, C., Malloy, K., Mansouri, D., Martinez, E., McClelland, H., McPherson, J., Mercadao, C., Metzker, M., Milosavljevic, A., Minja, E., Morgan, M., Morris, S., Munidasa, M., Murray, D., Nazarith, L., Ngo, D., Nguyen, N., Norwig-Eastaugh, E., Okwonu, G., Okwonu, K., Parker, D., Pasternak, S., Peatel, B., Patel, V., Paul, H., Perez, L., Perez, L., Petrosino, J., Pham, T., Primus, E., Pu, LL., Puazo, M., Qin, X., Quinn, A., Quircz, J., Rabata, D., Rachlinin, E., Reigh, R., Reht, Y., Reuter, M., Rohes, S., Rives, C., Rodriguez, F., Royas, A., Ruiz, S.J., Sana, M., Sanders, W., Santibanez, J., Sned, A., Sodergren, R., Songy, X, Sona, M., Krejos, Z., Usmani, K., Vargo, C., Verduzco, D., Villasana, D., Virk, D., Volkov, A., Waldron, L., Walker, B., Wang, S., Warren, J.,
Act Color Color	ATTACTORING ATTACTORITA ACTACTORITA ACTACT

COMMENT

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GI:9858994
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                                                                                                                                                                                                                                                                                                                Direct Submission

Submitted (13-JAN-2006) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jan 23, 2006 this sequence version replaced gi:74136772.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the fature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). ONDE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Wei,X., Wheeler,D., Williams,G., Williams,R., Worley,K., Wright,R., Ru,J., Yakub,S., Yan,K., Yuan,Y., Yu,F., Zhang,J., Zhang,L., Zhang,Z., Zhou,J., Weinstock,G. and Gibbs,R.A. Direct Submission
                                                                                                                                                              Direct Submission
Submitted (04-SEP-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 197215)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: Atlas 3.0;
Consensus quality: 193754 bases at least Q40
Consensus quality: 194610 bases at least Q30
Consensus quality: 195146 bases at least Q20
Estimated insert size: 199308; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of 1637 bp in length
gap of 50 bp
contig of 20861 bp in length
gap of 779 bp
contig of 22353 bp in length
gap of 402 bp
contig of 122800 bp in length
gap of 50 bp
contig of 9904 bp in length
gap of 50 bp
contig of 15508 bp in length
gap of 50 bp
contig of 15508 bp in length
gap of 50 bp
gap of 9904 bp in length
gap of 90 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195958: contig of inknown length
195958: contig of 1364 bp in length
59 195958: gap of unknown length
59 197215: contig of 1257 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Baylor College of Medicine
Center code: BCM
                                                                                                                                                                                                                                                                                                   Bovine Genome Sequencing Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: FMSU
Center clone name: CH240-216G5
------ Summary Statistics
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                                                                                                                    2 (bases 1 to 197215)
Worley, K.C.
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                                                                                                                    REFERENCE
AUTHORS
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JOURNAL
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143288 CACAAAGTTTCGTTCTGCCTGTCATCTACACTTTTAACA------TTCAGTTAGT 143240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143195 TGGGTATTTAATTGGTTAAACTAAATTTCCAAGGGAAAAATGAGATAGGCTGGTTGTTT 143136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143020 CAGTITIGCAAIGGIAIGGIIITAAIGCIGIGGIAAITIGIGAAAAIACCAIAGAGIIIT 142961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159859 bp DNA linear HTG 25-AUG-2000
Homo sapiens chromosome RPCI-11 clone RP11-707H2, WORKING DRAFT
SEQUENCE, 7 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143239 GAATGCATC------TAATTTAGTTTTGCTAAATAGGAAAATATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTATACTTTTAAATT----TTAAAAATTGAAATGACACTTGGAGTAACAATTGCCTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 ATAAATTTGAAAAAATGTTAACTACTCTGATAAAAAGTTTTATAGTTTTCCTACTTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 AAATAAATATTAAGCCTAGTAAGTATAATTTTAATATTGTCAAATAATTTGGAAAATACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      573 TGATTTAATAATGGTATGGAGTTAGGGCTATGATAATTAGTGAAAACACCCCAAGAATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              293 AGCAAAATTCCATAGGGCATGGTAATTGTAGTTTCAACATTACTTGCAGTTTCAGTTAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 197215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 24.0%; Score 168; DB 12; Length 19
Best Local Similarity 67.2%; Pred. No. 6.8e-39;
Matches 371; Conservative 0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             /estimated length=unknown
195859. .195958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'estimated_length=unknown
/organism="Bos taurus"
/mol_type="genomic DNA"
/db_xref="taxon:9913"
                                                                                                                                                               22549. .23327 /
/estimated length=779
45681. .46082
                                                                                                                                                                                                                                                 estimated_length=402
                                                                                                                                        /estimated_length=50
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178837. .178886
                                                                                                                                                                                                                                                                                                                                                             estimated length=50 194395. .194494
                                                                                  clone="CH240-216G5"
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PRI 08-OCT-2003
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4 (bases 1 to 172573)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 172573) Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC007276 172573 bp DNA linear PRI 08-C
Homo sapiens BAC clone RP11-22601 from 7, complete sequence.
AC007276
                                                                                                                                                                                                                                                                                                                                                          DB 12; Length 159859;
                                                                                                                                                                                                                                                                                                                                                        Score 115.6; DB 12; Length
Pred. No. 1.5e-23;
0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 172573)
Joshu,C., Le,T., Maupin,R. and Yoakum,M.
The sequence of Homo sapiens BAC clone RP11-22601
Unpublished (2001)
3 (bases 1 to 172573)
Waterston,R.H.
                                                    32214. .32313 —
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32314. .50864
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                                                                                                                  /estimated length=unknown
107063. .159859
/note="assembly_name:Contig14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae, Homo.

1 (bases 1 to 172573)

Sulston, J.E. and Wilson, R.

Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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                                                                                                                                                                                                    /estimated_length=unknown
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87.0%;
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                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 87.0
Matches 127; Conservative
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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AC007276
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                                                                                                                                                                                                 Direct Submission
Submitted (09-JUL-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Aug 21, 2000 this sequence version replaced gi:9857594.
                                                  Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5768: contig of 5768 bp in length
5868: gap of unknown length
16669: contig of 10201 bp in length
16169: gap of unknown length
32213: contig of 16644 bp in length
32313: gap of unknown length
50864: contig of 18551 bp in length
50864: gap of unknown length
74031: contig of 23067 bp in length
7431: gap of unknown length
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note="assembly_name:Contig8"
1769. .5868
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5869. .16069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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db_xref="texon:9606"
/chromosome="RPC1-1"
/clone="RP11-707H2"
                                                                                                                           The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                        ----- Genome Center
   HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                   Hominidae, Homo.
1 (bases 1 to 159859)
Waterston, R.H.
                                                                                                                                                                   2 (bases 1 to 159859)
Waterston, R.H.
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50864: 9
50964: 9
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                   sapiens (human)
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                 Homo sapiens
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                                                                                                                                                                                                                    /rpt_family="AT_rich"
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12902. 13156
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1057. :1183
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|192<u>4</u>.
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11586.
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360<u>6</u>.
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2175.
  repeat_region
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Exic D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University denome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GIB/CHR7, send mailto:egreen@nhgri.nih.gov or see http://genome.wustl.edu
Direct Submission
Submitted (30-SEP-2000) Department of Genetics, Washington
University, 4444 Porest Park Avenue, St. Louis, Missouri 63108, USA
6 (bases 1 to 172573)
                                                                                                         Direct Submission
Submitted (29-APR-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
7 (bases 1 to 172573)
                                                                                                                                                                                                                                    Submitted (08-OCT-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Dec 16, 1999 this sequence version replaced gi:5001518.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTICE: This sequence may not represent the entire insert of this forms. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 0); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The clone sequenced to the right is RPI1-332C7, 200 bp overlap. Actual start of this clone is at base position 1 of RPI1-22601 actual end is at base position 172379 of RPI1-22601. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                 Web site: http://genome.wustl.edu
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
Center project name: H.NH0226001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'organism="Homo sapiens"
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/clone_lib="RPCI-11"
1. .161
                                                                                                                                                                                                                                                                                                       -- Genome Center
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/rpt_family="MaLR"
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170. .282
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                                                                                                                                                                                                                  Direct Submission
                                                                                       Waterston, R.
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family="Alu"

family="Alu"

.11140

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family="MER1_type"

FEATURES

family="L1"

13900

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family="L1" .16463

repeat_region

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Center project name: L1162
Center project name: 45_I12
Center clone name: 45_I12
Center clone name: 45_I12
Center clone name: 45_I12
Sequencing vector: M13, M7815; 50% of reads
Sequencing vector: Plasmid; n/a; 50% of reads
Chemistry: Dye-primer-amersham; 2% of reads
Chemistry: Dye-primer-amersham; 2% of reads
Chemistry: Dye-terminator: B19_Dye; 9% of reads
Consensus quality: 146316 bases at least Q40
Consensus quality: 146316 bases at least Q40
Consensus quality: 147133 bases at least Q30
Consensus quality: 147173 bases at least Q30
Insert size: 142000; agarose-fp
Insert size: 142000; agarose-fp
Insert size: 147559; sum-of-contigs
Quality coverage: 11,4 in Q20 bases.
*NOTE: This is a "working draft' sequence. It currently
consists of 4 contigs. The true order of the pieces
*is not known and their order in this sequence record is
**This consists of the pieces of the present of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                         Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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vector_side:left"
28598. ..28697
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Silven, Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwill, J., Barna, N., Beckerly, R., Boqualavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Colangelo, M., Collins, S., Collymore, A., Colangelo, M., Domino, M., Donelan, L., Doyle, M., Ferreitz, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., McTewy, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vasalliev, H., Vo, A., Wheeler, J., Wu, X., W., McKern, D., Ye, W. J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X.,
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Homo sapiens clone RP11-45112, WORKING DRAFT SEQUENCE, 4 unordered
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Submitted (01-OCT-1999) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 147859)
1 Tren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-45112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 TTTTTTTTTTGATGATTTTAATAAAATATCATTTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.5%; Score 115.6; DB 5;
87.0%; Pred. No. 1.5e-23;
live 0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="(TAGA)n"
18052. 18542
180546. 26945
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268946. 26945
/rpt_family="(TA)n"
/rpt_family="(TA)n"
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/rpt_family="(TA)n"
                  7665. .17812
rpt_family="(TAGA)n"
7881. .18047
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AC011079.3 GI:11136801
HTG; HTGS_PHASE1; HTGS_DRAFT.
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28585..29070
/rpt_family="MalR"
29120..29280
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29332. .29516
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Matches 127; Conservative
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VERSION
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REFERENCE
AUTHORS
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AUTHORS
TITLE
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JOURNAL
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SOURCE
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Gaps

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NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Insert size: 168721; sum-of-contigs
Quality coverage: 5.0 in Q20 bases; agarose-fp
Quality coverage: 4.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                               7: contig of 1917 bp in length
7: gap of 100 bp
7: contig of 92 bp in length
7: gap of 100 bp
7: contig of 2255 bp in length
7: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136123: contig of 24571 bp in length
136223: gap of 100 bp
169821: contig of 33598 bp in length.
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[. .1917
'note="assembly_fragment"
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/note="assembly_fragment"
46860, .46959
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2210. 4464
/note="assembly_fragment"
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2849. .21008
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     169821 bp DNA linear HTG 28-MAR-2000
Homo sapiens chromosome 4 clone RP11-6901 map 4, WORKING DRAFT
SEQUENCE, 12 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAR 28, 2000 this sequence version replaced gi:7212073. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                  AAGTTTTAGGGTACATGTGCAAAGTGTGCAGGTTAGTTACATATATACATGTGCCATG
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Sequencing vector: M13; W77815; 100% of reads
Sequencing vector: M13; W77815; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 163347 bases at least Q40
Consensus quality: 1667964 bases at least Q30
Consensus quality: 167961 bases at least Q20
Insert size: 163000; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu------- Project_Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae, Homo.

1 (bases 1 to 16981)

1 Theren, B. Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 4, clone RP11-6901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seg.wi.mit.edu
                                                                                                                                                                                   89986 CTGGTATGCTGCACCCACTATCTC 90009
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                                                                                                                                                           CTGGTGTGCTGCACCCATTAACTC 161
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Homo sapiens (human)
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AC025490.2 GI:7331510
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                            DEFINITION
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VERSION
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JOURNAL
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AC025490
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f 100 bp g of 8184 bp in length f 100 bp g of 8160 bp in length

100 bp of 15698 bp in length 100 bp

100 bp of 9953 bp in length

18079 bp in length

100 bp

19447 bp in length

in length

100 bp of 26767 bp

100 bp



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source
                              TITLE
JOURNAL
   REFERENCE
                 AUTHORS
                                                                                                                                        JOURNAL
                                                                                           REFERENCE
                                                                                                          AUTHORS
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Homo sapiens BAC clone RP11-542P2 from 4, complete sequence.
AC093671
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Direct Submission
Submitted (07-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 53108, USA
4 (bases 1 to 186370)
Waterston, R. H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                         DB 12; Length 169821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 186370)
Holmes,A., Elliott,G. and Kozlowicz,A.
The sequence of Homo sapiens BAC clone RP11-542P2
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                      18;
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Sulston,J.B. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                       16.5%; Score 115.2; DB llarity 87.5%; Pred. No. 2e-23; Conservative 0; Mismatches 1
                                                                                                                                                                                             111453. .111552
/estimated length=100
111553. .136123
/note="assembly_fragment"
136124. .136223
/estimated_length=100
        46960. .65038
/note="assembly_fragment"
65039. .65138
                                                                                                                                                   /estimated length=100
84686. .111452
/note="assembly_fragment"
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                                                           /estimated_length=100
65139. .84585
/note="assembly_fragment
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estimated_length=100
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                                                                                                          clone_end:T7
vector_side:right"
                                                                                                                                                                                                                                                                                            136224. 1\overline{6}982\overline{1}
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                                              . .65138
                                                                                                                                        84586. .84685
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Waterston, R.
Direct Submission
Submitted (10-JAN-2002) Department of Genetics, Washington
Submitted (10-JAN-2002) Avenue, St. Louis, Missouri 63108, USA
On Dec 15, 2001 this sequence version replaced gi:16259163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MCP. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P. Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J. J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and Coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The clone sequenced to the left is AC048378; the clone sequenced to the right is RP11-5X16. Actual start of this clone is at base position 1 of RP11-542P2; actual end is at base position 186370 of
                                                        Direct Submission
Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 186370)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="match to EST BM021296 (NID:g16535652) ie75d01.y1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center project name: H_NH0542P02
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1. .186370
// organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="taxon:9606"
/chromosome="4"
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NEIGHBORING SEQUENCE INFORMATION:
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/rpt_family="Alu"
4. .22
5 (bases 1 to 186370)
Waterston, R.H.
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6969. .7019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 CTGGTGTGCTGCACCCATTAACTC 161
                                         /rpt_family="L2"
7595. .7693
/rpt_family="Alu"
7676. .7696
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1 (bases 1 to 212421)
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AC109591
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'note="match to EST BG940813 (NID:g14340185) ax07g01.rl"
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                                                                                                                                                                                                                                                                                                        (NID:93678721) qf34f05.x1"
                                                                                                                                                                                                                                                                                                                                    match to EST AA054948 (NID:g1547446) zf16d10.rl"
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5107. .5293
/note="match to EST AA909866 (NID:g3049156) ol09h06.s1"
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2747. 2829
7/note="match to EST BE243070 (NID:g9094804)"
2748. 2829
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'note="match to EST BG613633 (NID:g13665004)"
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2763. .2829
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/note="match to EST BG477315 (NID:g13409594)"
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/note="match to EST BG707099 (NID:g13983105)"
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/note="match to EST BI760964 (NID:g15752542)"
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                                                                                                                                                                                                                                                                      'note="match to EST BG566524 (NID:g13574177)"
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/note="similar to Homo sapiens BST BIS47286
(NID:915434598)"
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(NID:g15434598)"
                              note="match to EST AW137642 (NID:g6141960)
                                                                                                                        note="similar to Homo sapiens EST BE961990 [NID:911764436]"
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2769, .2829
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1437. .1657
/rpt_family="L1"
2190. .2192
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'note="match to EST
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/rpt_family="L1"
608. .710
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/rpt_family="L1"
1392. 1412
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/rpt_family="MIR"
4804. .5293
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/rpt_family="L1"
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212421 bp DNA linear HTG 09-FEB-2002
Homo sapiens chromosome 4 clone RP11-739KS, WORKING DRAFT SEQUENCE,
AC109591
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8231. 8304
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(NID:g15713364)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                   3231. .8304
/note="match to EST AI692905 (NID:94970245) wd42f12.x1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston, N.H.

Direct Submission
Submitted (05-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. On Feb 9, 2002 this sequence version replaced gi:18497268.
                                                                                                                                                                                                                                                                                                                                                                             Length 186370;
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7676_ 7696
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7743. .7997
/rpt_family="L1"
8221. .8304
0228. .8304
8228. .8304
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                                                                                                                                     8228. .8304
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8228. .8304
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                                                                                                                                                                                                                                                                                                                                                                         Query Match 16.5%; Score 115.2; DB 5; Best Local Similarity 87.5%; Pred. No. 1.9e-23; Matches 126; Conservative 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT09591.2 GI:18642962
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 TTTTTTTTTGATGATTTTAATAAAATATCATTTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence of Homo sapiens clone Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.5%; Score 115.2; DB 12; Length 212421; ilarity 87.5%; Pred. No. 1.9e-23; Conservative 0; Mismatches 18; Indels 0; G
             Sequencing vector: M13, 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 209891 bases at least Q40
Consensus quality: 210714 bases at least Q30
Consensus quality: 211269 bases at least Q20
Insert size: 190000; agarose-fp
Insert size: 212031; suu-of-contigs
Quality coverage: 7.60 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4750: contig of 4750 bp in length
4850: gap of unknown length
39482: contig of 34632 bp in length
39582: gap of unknown length
68572: contig of 28990 bp in length
68735: contig of 24063 bp in length
92735: contig of 24063 bp in length
131161: gap of unknown length
131261: gap of unknown length
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4851. .39482
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----- Summary Statistics
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4851
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39583
68573
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Best Local S
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Similarity

Matches 126;

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77

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Hominidae, Pan.

1 (bases 1 to 161343)
Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariaga, K.,
Chu, G., Coleman, B., Coleman, H., Engle, J., Granite, S., Guan, X.,
Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P.,
Hurle, B., Hold, J.R., Karlins, E., Kwong, P., Laric, P., Lee-Lin, S.-Q.,
Begapi, R., Madurc, Q.L., Madurcy, V.B., Margulies, E.H., Masiello, C.,
Maskeri, B., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E.,
Prasad, A., Reddix-Dugue, N., Schandler, K., Schueler, M.G., Shah, K.,
Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V.,
Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.
NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                 AC144869 161343 bp DNA linear HTG 09-JUN-2003
Pan troglodytes clone CH251-287A2, WORKING DRAFT SEQUENCE, 7
78 AAGTTTTAGGGTACATGTGCAAAGTGTGCAGGTTAGTTACATATATACATGTGCCATG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Assembly program: Phrap; version 0.990319
Consensus quality: 160248 bases at least Q40
Consensus quality: 160506 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-MAY-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 161343)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-JUN-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Jun 9, 2003 this sequence version replaced gi:31044282.
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Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
                                                                                                                                                              93520 CTGGTATGCTGCACCCACTATCTC 93543
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Center clone name: 287A02
                                                                                                                               CTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS PHASE2; HTGS DRAFT.
Pan troglodytes (chimpanzee)
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC144869.2 GI:31544080
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                           ordered pieces.
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                                                                                                                               138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
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JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
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TCACATAAAGTTTTTTTTTTTGATGATTTTAATAAAATATCATTTTCTTTTTTTATTAT

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77287 TATTATACTITITAAGTITITAGGGTACATGTGCACAATGTGCAGGTTAGTTACATATGTAT 77346

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provided by the submitter.

This sequence will be replaced

by the finished sequence as soon as it is available and

the accession number will be preserved.

1 55269 Contig of 25268 bp in length

25369 40449; contig of 15081 bp in length

40450 47926; contig of 15081 bp in length

40550 47926; contig of 7377 bp in length

40550 47926; contig of 7377 bp in length

40570 40929; contig of 7377 bp in length

55498 55597; contig of 36830 bp in length

55598 9527; contig of 36830 bp in length

92428 9527; gap of unknown length

92528 96210; contig of 36830 bp in length

92528 96210; contig of 3683 bp in length

92531 96310; contig of 65033 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="clone overlaps with GenBank Accession Number AC099408 clone RP43-44D23 (center project name cmb)"
                                                                                                                                                                 consists of 7 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                   Insert size: 178000; agarose-fp
Insert size: 160743; sum-of-contigs
Quality coverage: 10 74x in Q20 bases; agarose-fp
Quality coverage: 11.89x in Q20 bases; sum-of-contigs
                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently
Consensus quality: 160675 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .161343
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47927. .48026
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Submitted (09-JAN-2002) Department of Genetics, Washington Submitted (09-JAN-2002) Department of Genetics, Mashington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 00); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (12-ULL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. 3
MO 63108, USA
5 (bases 1 to 135692)
                                                                                                                                                         ACO21134 135692 bp DNA linear PRI 09-JJ
Homo sapiens BAC clone RP11-402D23 from 4, complete sequence
ACO21134
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On Jul 12, 2001 this sequence version replaced gi:14573744.
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Center code: WUGSC
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                            77347 ACATGTGCCATGCTGGTATGCTGCACCCATTAACTC 77382
126 ACATGIGCCATGCTGGTGTGCTGCACCCATTAACTC 161
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Contact: sapiens@watson.wustl.edu
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Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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Waterston, R.H.
Direct Submission
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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Score 114.4; DB 12; Length 161343; Pred. No. 3.4e-23; 0; Mismatches 26; Indels 0; G

16.3%; illarity 83.3%; Conservative (

Query Match Best Local Similarity Matches 130; Conserv

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Length 135692;
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23552..23596
'rpc_family="(GAA)n"
23636..23835
'rpc_family="L1"
24614..24707
'rpc_family="L2"
25286..25758
'rpc_family="ERVL"
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17208. 17256
/rpt family="(TATG)n"
21435. 21631
                                                                                                                                           /rpt_family="MIR"
21610. 21637
/rpt_family="AT_rich"
21750. 21820
/rpt_family="AT_rich"
21864. 22532
/rpt_family="ERV1"
23064. 23053
/rpt_family="ERV1"
23064. 23053
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/rpt_family="ERVL"
26291. .26313
/rpt_family="AT_rich"
2775. .28061
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27861. 27884
/rpt_family="(A)n"
28036. .28062
/rpt_family="(GAA)n"
28108. .28660
28108. .28660
28898. .29396
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/rpt_family="AT_rich"
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15073. .15665
/rpt_family="ERVL"
15708. .16234
/rpt_family="ERVL"
16344. .16645
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/rpt_family="ERVL"
29857. .30047
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30674. .30965
/rpt_family="L2"
31191. .31434
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36190..3663
/rpt_family="L1"
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36826. .36956
/rpt_family="L1"
37137. .37158
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17447. .37472
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2080. .32373
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34203. .34248
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12660. .32718
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                                                                                                                                      The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and Coworkers at the Roswell Park Cancer Institute
                                             Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                       VECTOR: pBACe3.6
BIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is AC005150, 2000 bp overlap.
Actual end of this clone is at base position 135692 of RPII-402D23.
                                                                                                                                                                                                                                                                                                                                                      Polymorphisms have been identified between AC005150 and RP11-402D23.
                                                                                                                                                                                                                                                                                                                                                                                                         1. .135692
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="4"
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219. .2247
rpt_family="(T)n"
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clone_lib="RPCI-11"
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rpt_family="(ATG)n"
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rpt_family="(TA)n"
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1545. .11707
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12184. .12212
/rpt_family="(A)n"
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rpt_family="ERVL"
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2. .532
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'rpt_family="Alu"
1476. .1154
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rpt_family="MIR"
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'208, '70er
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                                                                                                                                           AC116177 156393 bp DNA linear HTG 25-MAR-2002 Homo sapiens chromosome UNK clone RP11-527M7, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.
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1 (bases 1 to 156393)
Waterston,R.H.
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  Gaps
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20; Indels
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Waterston, R.H.
Direct Submission
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Homo sapiens
Matches 137; Conservative
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Mammaliae; Homo.

It (bases 1 to 154369)

Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Buncoks, S., Brieva, M., Bryant, N.P., Burch, P., Burketl, C., Burrell, K.L., Bryd, N.C., Carron, T.F., Carrer, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, Z., Chiu, D., Dathorne, S.R., Davia, M., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.J., Dragber, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Emerling, S., Escotto, M., Falls, T., Gao, J., Garcia, A., Garner, T., Garzer, P., Frantz, P., Gabisi, A., Gavara, A., Garner, T., Garzer, P., Frantz, P., Gabisi, A., Gavara, A., Garner, T., Haves, A., Harris, C., Harris, K., Hart, M., Havlak, P., Hamilton, K., Hani, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hamilton, K., Hani, J., Harris, C., Harris, K., Hart, M., Havlak, P., Johnson, R., Jolivet, S., Joudeh, S., Karlsson, B., Yais, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, B., Yais, Y., Lucier, A., Lucier, R., Luna, R., Martin, 
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Homo sapiens 12 BAC RP11-359B12 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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July 19, 2006, 06:41:39; Search time 517 Seconds (without alignments) 9440.182 Million cell updates/sec
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Description	Ady94258 BRAF prot	Aal05340 Human rep	Ab198209 Human tes	Aba19101 Human ner	Adq59197 MSI-H car	Adj12500 DNA fragm	Aas46305 Tumour su	Abl32396 Human imm	Abk34008 Human DNA	Abq67177 Human ang	Adb54111 Pretreate	Adb54239 Pretreate	Ade84177 Human lym	Ade84101 Human lym	Ads89541 Oligonucl	Ads89267 Oligonucl	Ado48201 Human p21	Abv72623 Human tra
ID	4 ADY94258	AAL05340	ABL98209	ABA19101	2 ADQ59197	2 ADJ12500	AAS46305	ABL32396	ABK34008	ABQ67177	0 ADB54111	10 ADB54239	0 ADE84177	0 ADE84101	3 ADS89541	3 ADS89267	2 ADO48201	ABV72623
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B-Raf protein kinase; melanoma; cytostatic; diagnosis; DNA polymorphism; drug screening; chromosome-7q34; gene therapy; BRAF; ds; gene; single nucleotide polymorphism; SNP.

Homo sapiens

BRAF protein kinase gene DNA sequence.

16-JUN-2005 (first entry)

ADY94258;

ADY94258 standard; DNA; 190276 BP.

RESULT 1 ADY94258

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Identifying a subject at risk of melanoma, useful for treating or preventing melanoma by detecting the presence or absence of one or more polymorphic variations associated with melanoma in a nucleic acid sample

The new invention relates to the discovery that polymorphic variations in a gene (ADY94258) encoding a BRAF protein kinase is associated with the occurrence of melanoma. BRAF is a serine/threonine protein kinase and is a member of the RAF family. It participates in the RAF/RAF/MEK/ERK/MAP kinase signal transduction pathway. The BRAF gene is located on chromosome 7q34 (assembly 30). Provided are methods of identifying a pubject at risk of melanoma by detecting the presence or absence of one or more polymorphic variations in BRAF associated with melanoma in a nucleic acid sample from a subject. Also disclosed is a method of an incident polymorphic variation associated with melanoma. Also disclosed is a method of an incident polymorphic variation associated with melanoma. Also disclosed is a method of identifying a candidate molecule that modulates cell proliferation by introducing a test molecule to a system which

comprises the nucleic acid; and determining the presence or absence of an interaction between the test molecule and the nucleic acid or protein. The polymorphic variations are detected at one or more positions in a DV94258. The positions are in linkage disequilibrium with one or more positions in SEQ ID No. 1, or the variation is the haplotype CTTG or ATGA in ADV94258. Detecting the presence or absence of the one or more polymorphic variations comprises hybridizing an oligonuclectide to the nucleic acid sample, where the oligonuclectide hybridizes to a region adjacent to the polymorphic variation. The proximal polymorphic variation is within a region between about 5 kb 3' of the incident polymorphic variation or variation and about 5 kb 3' of the incident polymorphic variation contact and about 5 kb 3' of the incident polymorphic variation.

Treating melanoma in a subject alternatively comprises contacting one or more cells of a subject with a duplex RNA nucleic acid. The invention is useful for treating or preventing melanoma. The present sequence is the DNA sequence of the human BRAF gene. 146060 146120 146300 146360 146420 146480 ö 180 120 300 360 480 Sequence 190276 BP; 55599 A; 35097 C; 37143 G; 62425 T; 0 U; 12 Other; 146001 CIGTITCACATAAAGITITITITITITITITGATGATTATAAAAATATCATITITITITIT 146181 TTTTAGTGACAGTTTTAGTCATTTTCCTAATTGAAAGTATCATAAGTAATCTAAATTT 121 TATATACATGTGCCATGCTGTGTGCTGCACCCATTAACTCACATGAAGTTTTTTTAAA TITIAGIGACAGITITIAGICATITICCIAATIGAAAGIATCATAAGIAATCCATAAATTT GAAAAAAATGTTAACTCTGATAAAAAAGTTTTATAGTTTCCTACTTTAAGCAAAAT 146421 TAATTGATTTTACCAAATTTCCATGGAACAAGCAAGGTTGGCTATTTTTGGATTGATAT 541 GGAGTTTAGATAGCTAAAGTATAATTTTATTTGTGATTTAATAATGGTATGGAGTTAGGGC ATTAAGCCTAGTAAGTATAATTTAATATTGTCAAATAATTTGGAAAATACCATGGGTACT TAATTGATTTTACCAAATTTCCATGGAACAAACAAGGTTGGCTATTTTTGGATTGATAT TITGAAATACTAGTACAGGAATATCATTGTTAGTTGAATTTTTAGCCTTAGAAAACAAAT Gaps DB 14; Length 190276; .. 0 Indels Match 100.0%; Score 700; DB 14; Local Similarity 99.9%; Pred. No. 5e-110; es 699; Conservative 1; Mismatches 0; 241 361 421 181 301 61 481 Query Match Best Loca Matches g g g g g Q ò Dp ò ò ద ò δ 유 ò ò ò ò

RESULT 2 AAL05340/c

146661 TGACACTTGGAGTAACAATTGCCTTTTTAGGTGATGTGGCA 146700 TGACACTTGGAGTAACAATTGCCTTTTAGGTGATGTGGCA

661

601 TATGATAATTAGTGAAAACACCCAAGAATGTTTTATACTTTTAAAATTTAAAAATTGAAA

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Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
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02-OCT-2000;
02-OCT-2000;
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16-MAR-2000;
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19-MAY-2000;
07-JUN-2000;
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23-AUG-2000;
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    10049 ATTATTATACTTTTAAGTTTTAGGGTACATGTGCACAACGTGCAGGTTTGTTACATATGT 9990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
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04-FEB-2000; 2000US-0180628P.
02-MAR-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0186659P.
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Best Local Similarity 82.3
Matches 130; Conservative
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Ruben SM (HUMA-) HUMAN GENOME SCI INC. Rosen CA, Barash SC,

Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer. WPI; 2001-483232/52.

The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The Disclosure; SEQ ID NO 2861; 766pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a protein fragment of the invention
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14-AUG-2000; 2000US-0225213P.
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24-FEB-2000;
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26-JUL-2000;
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2000US-0233063P.
2000US-0233064P.
2000US-0233065P.
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2000US-0230437P.
2000US-023143P.
2000US-0231243P.
2000US-0231244P.
2000US-0231244P.
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2000US-0229343P.
2000US-0229344P.
2000US-0229345P.
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2000US-0236367P.
2000US-0236368P.
                                     2000US-0225759P
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2000US-0232080P
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              14-AUG-2000;
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22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
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05-889-2000;
06-889-2000;
06-889-2000;
08-889-2000;
08-889-2000;
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08-NOV-2000
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08-NOV-2000; 2000US-0246526P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246653P.
08-NOV-2000; 2000US-0246609P.
08-NOV-2000; 2000US-0246611P.
08-NOV-2000; 2000US-0246611P.
17-NOV-2000; 2000US-0249208P.
17-NOV-2000; 2000US-0249208P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-0249264P.
17-NOV
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2000US-0251030P.
2000US-0251988P.
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2000US-0251868P.
2000US-0251869P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-DEC-2000; 2
05-DEC-2000; 2
06-DEC-2000; 2
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Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases. WPI; 2001-541565/60

Rosen CA, Barash SC, Ruben SM

Disclosure; SEQ ID NO 11432; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating comedical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, constant cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointeetinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, commultiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as wyccardial ischaemias; (d) wound healing confections diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 19167 BP; 5592 A; 3875 C; 3876 G; 5824 T; 0 U; 0 Other;

2000US-0246524P

08-NOV-2000;

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9119 ATTATTATATCTTTTAAGTTTTAGGGTACATGTGCACAACGTGCAGGTTTGTTACTTATATGT 9178
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                                                                                                  9059 Tranaactaacrititititititititigieseriesaaarcritititititaarititair 9118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeats (CMNRS). The genes are useful for the development of an antibody against MSI-H (hugh microsatellite instability) tumour. Also described: [1] cDNA genes containing cMNRs with 10 or more nucleotide sequences, and selected from the cDNA genes having the nucleotide sequences of SEQ ID NOS:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41 and 41; (2) cDNA genes, which are frameshift mutated by deletion or insertion of one or more base in the cMNRs; (3) genomic DNA genes containing cMNRs with 10 or more nucleotide sequences, and selected from the genomic DNA genes having the nucleotide sequences of SEQ ID NOS:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42 and 44; and (4) genomic DNA genes, which are frameshift mutated by deletion or insertion of one or more base in the cMNRs. The genes have cytostatic activity. The present sequence represents an MSI-H carcinoma genomic DNA sequence from the present invention.
                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes containing coding mononucleotide repeats are useful in developing an antibody against MSI-H (hugh (sic high) microsatellite instability)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes genes containing coding mononucleotide
                                                                    'TTTTTTGATGATTTAATAAAATATCATTTTCTTTTTTATT
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              coding mononucleotide repeat, cMNR; gene, antibody, MSI-H tumour; MSI-H carcinoma; high microsatellite instability tumour; high microsatellite instability carcinoma; cytostatic; ds.
                                     ;
0
 Length 19167;
                                   28; Indels
                                                                                                                                                                                                                                     9179 ATACATGTGCCATGTTGGTGCTGCACCCATTAACTC 9216
                                                                                                                                                                                                       124 ATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                               MSI-H carcinoma genomic DNA sequence SEQ ID NO:34.
 DB 5;
   Score 113.2; DB 5
Pred. No. 2.1e-10;
                                 0; Mismatches
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                                                                                                                                                                                                                                                                                                                      ADQ59197 standard; DNA; 155225
16.2%;
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                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim HG, Kim NG, Lee JS,
                                                                   4 TTTCACATAAAGTTTT"
                                   Conservative
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                 Similarity
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KIM N G.
LEE J S.
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                 Best Local Simi
Matches 130;
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   Query Match
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(LEEJ/)
(RHEE/)
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human; secreted; cancer; haematopoietic disease; anaemia;
multiple myeloma; reproductive system disorder; prostatitis;
multiple myeloma; reproductive system disorder; prostatitis;
inquinal hernia; musculoskeletal disease; systemic lupus erythematosus;
kW inquinal hernia disease; arrhythmia; hypernatraemia; fetal disease;
gout; cardiovascular disease; arrhythmia; hypernatraemia; fetal disease;
kW incontinence; renal disorder; neural; sensory disease;
kW alzheimer's disease; meningitis; respiratory disease;
kW alzheimer's disease; endocrine disease; emphysema;
cocupational lung disease; endocrine disease; scleroderma;
kW pidermolysis bullosa; cytostatic; antianemic; antianthritic;
antiasthmatic; anti-HIV; immunosuppressive; antianflammatory;
kW antisoriatic; antibacterial; osteopathic; dermatological; antispenic;
kW immunomodulator; antiarrhythmic; cardiant; nootropic; antilipemic;
kW mutidiabetic; antibacterial; osteopathic; dermatological; antilipemic;
kW mutidiabetic; antibacterial; osteopathic; antiparkinsonian; tranquilizer;
methrotropic; uropathic; hypertensive; vulnerary; ds.
                                                                                                        138520 ATTATTATACTTTTAAGTTTTAGGGTACATGTGCACAACGTGCAGGTTTGTTACATATGT 138579
                                                            ö
                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                            DNA fragment of a BAC clone that encodes a human secreted protein Seq354.
                                                                                        4 TITCACATAAAGITITITITITITIGAIGATITITAATAAAATAICATITITITITITITITI
Sequence 155225 BP; 44334 A; 29321 C; 30431 G; 51139 T; 0 U; 0 Other;
                                                            Gaps
                              Length 155225
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0
                                                        28; Indels
                                                                                                                                                                                                                                         138580 ATACATGTGCCATGTTGGTGCTGCACCCATTAACTC 138617
                                                                                                                                                                                                           ATACATGTGCCATGCTGGTGTGCTGCACCATTAACTC 161
                            Score 113.2; DB 12;
Pred. No. 2e-10;
                                                          0; Mismatches
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97US-0061529P.
97US-0061532P.
97US-0061536P.
97US-0071498P.
98WO-US021142.
98WO-US021142.
                            16.2%;
                                                                                                                                                                                                                                                                                                                    ADJ12500 standard; DNA; 8766
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                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                          Matches 130; Conservative
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FLORENCE K A
GREENE J M.
YOUNG P E.
FERRIE A M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BREWER L A.
DUAN R D.
                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JS2004010132-A1.
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09-OCT-1997;
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                              Query Match
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(RUBE/)
(FLOR/)
(GREE/)
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(FERR/)
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                                                                                                                                                                                                                                                                                      RESULT 6
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This invention relates to novel polynuclectides encoding human secreted proteins. Specifically, it refers to the vectors, host cells, recombinant and synthetic methods for producing human polynucleotides, polypeptides and antibodies. Furthermore, it relates to screening methods to identify agonists and antagonists that can be used to inhibit or enhance the production and function of the secreted proteins. The present invention corrections of the secreted proteins. The present invention provouction and function of the secreted proteins. The present invention corrections as cancer, haematopoietic diseases including proventing disorders buch as cancer, haematopoietic diseases including protein inquinal hernia, musculoskeletal diseases including protein inquinal hernia, musculoskeletal diseases including carrinary incontinence and renal disorders, neural or sensory disease including archyphmia and hypernatraemia, mixed fetal diseases including fetal alcohol syndrome and bown's syndrome, excretory diseases including curinary incontinence and renal disorders, neural or sensory disease including diabetees and gomerulonephritis, respiratory disease including portal hypertension and irritable bowel syndrome and connective tissue or cipithelial diseases including scleroderms and connective tissue or cipithelial diseases including carritable bowel syndrome and connective tissue or cipithelial diseases including carritable disease, and anti-arritable diseases unclaimed and pomerulonephritis, digestic anti-arritable.

CC antiarritic, antispout, immunodoulator, antiarrhythmic, autispout, immunodoulator, antiarrhythmic, antispout, immunodoulator, antiarrhythmic, antispout, immunodoulator, antiarrhythmic, antispout, immunodoulator, antiarrhythmic, antispout, antippout, immunodoulator, antiarrhythmic, antispout, immunodoulator,
                                                                                                                                                                                                                                       New isolated nucleic acids and polypeptides, useful for diagnosing, treating, preventing or ameliorating diseases or disorders e.g. cancer, anemia, arthritis, asthma, inflammatory bowel disease or Alzheimer's
                                                                                                                Greene JM;
                                                                                                                                         Ebner R, Olsen H;
                                                                                                                Florence KA,
                                                                                                              Duan RD, Ruben SM,
Yu G, Florence C,
                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 354; 286pp; English,
                                                                                                                Brewer LA,
Ferrie AM,
                                                                                                                                                                                        WPI; 2004-090518/09
(FLOR/) FLORENCE C.
(EBNE/) EBNER R.
(OLSE/) OLSEN H.
                                                                                                              Rosen CA,
Young PE,
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ö 0; Gaps DB 12; Length 8766; Sequence 8766 BP; 2308 A; 1479 C; 1597 G; 3382 T; 0 U; 0 Other; / Match
Local Similarity 94.1%; Pred. No. 2.6e-09;
les 111; Conservative 0; Mismatches 7; Indels Query Match

44 TATCATTTTCTTTTTTATTATTATTATACTTTTAAGTTTTTAGGGTACATGTGCAAAGTG 103 61 104 TGCAGGTTAGTTACATATATACATGTGCCATGCTGGTGTGCTGCTGCTCTAACTC 161 recassitastracarareraracarsiscoarscrestarscrescentraacre 119 TTTTATTTTTATTTTTTATTATTATTATACTTTTTAAGTTTTTAGGGTACATGTGCACAATG N 62

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AAS46305 standard; DNA; 8666 AAS46305; RESULT 7 AAS46305 XXEXEX XXXXX

ВЪ

Tumour suppressor gene derived chemically modified sequence #27

(first entry)

18-DEC-2001

Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;

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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes bisulphite, of genes associated with tumour suppression and oncogenes busing from the sequence litting) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oilgomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleide polymorphisms and also to be used in an array for analysing probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therappy of existing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or epigenetic parameters, the differences serving as basis for diagnosis and/or epigenetic parameters, the differences serving as basis for diagnosis and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 513 genomic sequences detain electricia control form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1726 GITATITITITITITITITITITATATAAGATITATAATGGATAATGGATTITIATITIT 1785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1667 GTTATGTTGGTGTTGTTTTATTTATTTA-TTATTTAGTATTAGGTATATTTAAT 1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 GCCATGCTGGTGCTGCACCCATTAACTCACATGAAGTTTTTTTAAATTTTAGTGACA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 ACTITITAAGITITIAGGGIACAIGIGCAAAGIGIGCAGGITAGITACATATATATACAIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 GITITAGICATITICCIAAITGAAAGIATCATAAGIAAICCATAAAITTIGAAAAAAAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 8666;
tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 324; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 106.6; DB 4;
Pred. No. 2.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 27; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                 Berlin K;
                                                                                                                                                                                                                                   15-MAR-2000; 2000DE-01013847.
06-APR-2000; 2000DE-01019058.
07-APR-2000; 2000DE-01019173.
30-JUN-2000; 2000DE-01043826.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                               5-MAR-2001; 2001WO-EP002955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 15.2%;
Local Similarity 49.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 312; Conservative
                      cytosine methylation; ds
                                                                                                                                                                                                                                                                                                                                                                                                            Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                      (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-602752/68
                                                                                                            WO200168912-A2.
                                                                 Homo sapiens
                                                                                                                                                    20-SEP-2001.
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                                                                 2026 TTTAGAGAAATTTTGAATTTATTGAAGGTTTTAGTAAATATATGTGTAAGTGAATA 2085
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                                                                                                                                                                                                                                                                                                                                                                                                       491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene;
TAACTACTCTGATAAAAAGTTTTATAGTTTCCTACTTTTAAGCAAAATTCCATAGGGCA
                                                                                                                                                                                                                                                                    TAAGTATAATTTAATATTGTCAAATAATTTGGAAAATACCATGGGTACTTAATTGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1966 GTTATATATATATATAAGAGTTGAAAGAGTTTTTGATGTAGGAATTTATGGTAGGT
                                                                                                                                  312 TGGTAATTGTAGTTTCAACATTACTTGCAGTTTCAGTTAGTAAATATAAGCCTAG
                                                                                                                                                                                                                                                                                                                                                                                                432 ACCAAATTICCAIGGAACAAAGAIGGITGGCIATITITIGGAITGAIAITITGAAAIACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             552 AGCTAAAGTATAATTTATTTGTGATTTAATAATGGTATGGAGTTAGGGCTATGATAATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiarteriosclerotic, antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immune system disease; cytosine methylation; antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune system associated gene SEQ ID NO: 369.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGAAAACACCCAAGAATGTTTTATACTTTTAAATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL32396 standard; DNA; 8666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAAGTATAATTTAATATTGTCAAATAATTTGGAAAATACCATGGGTACTTAATTGATTT 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, ds; astrocytoma, cytostatic; staging, cysteine methylation; CpG; bisulphite; brain tissue; MALDI; ESI; electron spray mass spectrometry; matrix assisted laser desorption/ionization mass spectrometry.
                                     acute myeloid
can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumacoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                       1607 TATTTTAAGTTTTAGAGTATATGTGTATATGTGTAGGTTTGTTATATATGTATATGT
                                                                                                                                                                                                                                                                                                             72 ACTITITAAGITITIAGGGIACAIGIGCAAAGIGIGCAGGIIAGIIACAIAIAIATACAIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTTTAGTCATTTTCCTAATTGAAAGTATCATAAGTAATCCATAAATTTTGAAAAAAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              552 AGCTAAAGTATATTTATTTGTGATTTAATAATGGTATGGAGTTAGGGCTATGATTA
                                                                                                                                                                                                     1;
                                                                                                                                                                 DB 6; Length 8666;
                                                                                                                                Sequence 8666 BP; 2444 A; 168 C; 1868 G; 4186 T; 0 U; 0 Other;
                                                                                                                                                                                Pred. No. 2.9e-09;
0; Mismatches 324; Indels
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                                                                                                                                                            / Match 15.2%; Score 106.6; Local Similarity 49.0%; Pred. No. 2.9e les 312; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human DNA for staging of Astrocytomas #48.
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1726 GITATITITITITITITITITITATATAGATITIATAATGGATAATGGATITITATTIT 1785

GTTTTAGTCATTTCCTAATTGAAAGTATCATAAGTAATCCATAAATTTGAAAAAATGT

192

GCCATGCTGGTGCTGCACCCATTAACTCACATGAAGTTTTTTTAAATTTTAGTGACA 191

132

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1667 GTTATGTTGTTGTTTTTATTAATTTA-TTATTTAGTATTAGGTATATTTTAAT

252 TAACTACTCTGATAAAAAAGTTTTATAGTTTCCTACTTTTAAGCAAAATTCCATAGGGCA

ò ద 312 IGGIAATIGIAGITICAACATIACIIGCAGITICAGITAGIAAATAAATATAAGCCTAG

431

1906 TITATAATGIATITAAATGITGITITTATAGGITGIAITTITITATTATTATAATA 1965

432 ACCAAATTTCCATGGAACAAACAAGGTTGGCTATTTTTTGGATTGATATTTTGAAATACT

1966 GTTATATATATTTTTATAAGAGTTGAAAGAGTTTTTGATGTAGGAATTTATGGTAGAGT

TAAGTATAATTTAATATTGTCAAATAATTTGGAAAATACCATGGGTACTTAATTGATTTT

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ABQ67177 standard; DNA; 8666

RESULT 10 ABQ67177

552 AGCTAAAGTATAATTTATGTGATTTAATAATGGTATGGAGTTAGGGCTATGATAATTA

2026 TTTPAGAGAAATTTTTGAATTTTATTGAAAGTTTTAATTTAGAAATATATGTGAAGTGAATA 2085

492 AGTACAGGAATATCATTGTTAGTTGAATTTTTAGCCTTAGAAACAAATGGAGTTTAGAT

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Novel chemically modified genomic DNA sequences, useful in the characterization, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas or predisposition to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.2%; Score 106.6; DB 6; Length (ilarity 49.0%; Pred. No. 2.9e-09; Conservative 0; Mismatches 324; Indels
                                                                                                                                                   Claim 1; SEQ ID NO 95; 37pp; English
                                                                                    Berlin K;
                                  02-JUL-2001; 2001WO-EP007538.
                                                  30-JUN-2000; 2000DE-01032529
                                                       01-SEP-2000; 2000DE-01043826
                                                                                    Piepenbrock C,
                                                                      (EPIG-) EPIGENOMICS AG
                                                                                                  WPI; 2002-171649/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 312; Conserv
      WO200202808-A2
                                                                                                                                       astrocytomas.
                    10-JAN-2002
                                                                                    Olek A,
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The invention relates to a nucleic acid comprising a sequence (I) of at least 18 bases in length of a segment of chemically pre-treated genomic CC least 18 bases in length of a sequences of (ARX31919-ARX3402) or its complement. Also included are an oligomuclectide or peptide nucleic acid (or set thereof) of at least 9 nucleotides which hybridises to (I), probes for detecting cytosine methylation or single-conclected polymorphisms (SNP) in (I), an array of oligomers or peptide nucleic acids for analysing diseases associated with the methylation of states of the CpG dinucleotides of (I). The array is useful for determining genetic and/or epigenetic parameters, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas, or the predisposition to astrocytomas by analysing cytosine (a strocytomas, or the predisposition to astrocytomas by analysing cytosine methylations, involves obtaining a biological sample containing genomic DNA, extracting the genomic DNA, converting the genomic DNA, extracting the genomic DNA, converting the genomic DNA fragments using the array and a polymerase, where the another base which is dissimilar to cytosine in terms of hybridisation containing methylation status of one or more cytosine positions, and analysing methylation status of one or more data sets. The genomic DNA is chemically treated by using a blanlificate multifice or disulphite. The amplification status of the analysing methylation status of the constitution status of brain the specific genomic methylation status of brain cissue, based on the specific genomic methylation status of brain cissue, based on the specific genomic methylation status of the amplificates are detechable molecule fragments having a typical mass constitution and analysing methylation are detected in a mass spectrometer. The requestion status of the amplificates are detectable molecule fragments and entering an analysing methylation are detected in a mass spectrometer. The requestion of the specific parameters is a spect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pre-treated genomic DNA to be amplified, have a single positive or angative charge for a better detectability in the mass spectrometer. Preferably, the amplificates or fragments of the amplificates are detected by matrix assisted laser desorption/ionization mass spectrometry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              form part
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(WALDI) or using electron spray mass spectrometry (ESI). The present sequence is one of the chemically pre-treated reference DNA samples of the invention. Note: The sequence data for this patent did not form par of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                       directly from WIPO at ftp.wipo.int/pub/published pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8666 BP; 2444 A; 168 C; 1868 G; 4186 T; 0 U; 0 Other;
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Human; angiogenesis; methylation; eye disease; glaucoma; tumour; inflammation; rheumatoroid arthritis; disbetic retinopathy; antiulcerds; macular degeneration; inflammativs bowel disease; Crohn's disease; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; New nucleic acid fragments from chemically treated angiogenesis-36-DEC-2001; 2001WO-EP014320 06-DEC-2000; 2000DE-01061338 antiarteriosclerotic, ds (EPIG-) EPIGENOMICS AG VPI; 2002-500450/53. WO200246454-A2 Homo sapiens Schacht 0;

Human angiogenesis associated polynucleotide SEQ ID NO 207.

(first entry)

28-AUG-2002

ABQ67177;

426, App 454, App 15703, A 16066, A 150430,

Sequence

13420, A 12611, A 14413, A 15473, A 13404, A 16065, A

550, App 455, App 342, App 15744, A 3, Appli 3, Appli

sequence seq

12614, A 16061, A 13027, A 14577, A

59509, A 59510, A

360, App 32, Appl 38, Appl 13828, A 11542, A 11730, A 11730, A 117182, A 117

Sequence Sequence Sequence Sequence

468, App 16065, A 13675, A 12386, A

Sequence Sequence

Sequence Sequence Sequence

Sequence Sequence

Sequence Sequence Sequence

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; Sequence 77443, Application US/09949016
; Patent No. 6812339
; Batent No. 681239
; Fatent No. 681239
; Fatent No. 681239
; TITLE OF INVENTION:
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REPERBLOG: CLOO1307
; CURRENT FILING DATE: 2000-04-14
; FRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-30
; PRIOR FILING DATE: 2000-10-30
; PRIOR FILING DATE: 2000-10-30
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 77443
       US-09-984-429-4524
US-09-984-129-4524
US-09-949-016-150430
US-09-949-016-150430
US-09-949-016-134120
US-09-949-016-134120
US-09-949-016-13413
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US-09-949-016-13675
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 RESULT 1
US-09-949-016-77443
 Sequence 354, App
Sequence 1499, App
Sequence 12822, A
Sequence 15524, A
Sequence 15324, A
Sequence 2044, Ap
Sequence 2044, Ap
Sequence 703, App
Sequence 448, App
Sequence 448, App
Sequence 13133, A
Sequence 622, App
Sequence 13133, A
Sequence 13133, A
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Sequence 14000, A
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6821.751 Million cell updates/sec
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1 ctgtttcacataaagtttt.....gccttttaggtgatgtggca
                                                                July 19, 2006, 06:56:58; Search time 192 Seconds
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-949-016-134975

US-09-949-016-13524

US-09-949-016-13358

US-09-949-016-13358

US-09-949-002-2045

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US-09-949-002-1033

US-09-949-002-1033

US-09-949-016-13554

US-09-949-016-13654

US-09-949-016-13654

US-09-949-016-12415

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US-09-949-016-125970

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Maximum Match 100%
Listing first 70 summaries
                                             - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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ORGANISM: Homo sapiens
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US-09-984-429-469/C
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Sequence 14000, Application US/09949016
Fatent No. 681239
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                                                                                                                                                                                                        Indels
                                                                                                                                   16.0%; Score 112.2; DB 3; llarity 84.6%; Pred. No. 3.9e-13; Conservative 0; Mismatches 23;
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16.0%; Score 112.2; DB 3;
Best Local Similarity 84.6%; Pred. No. 4.9e-13;
Matches 126; Conservative 0; Mismatches 23;
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US-09-984-429-354
i Sequence 354, Application US/09984429
j Fatent No. 7026447
j GENERAL INFORMATION:
j APPLICANT: Rosen et al.
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LOCATION: (1)...(154626)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                             13 AAGTTTTTTT
                                                                                                                                                                    Best Local Similarity
Matches 126; Conserv
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FEATURE:
                                    , ORGANISM: Human
US-09-949-016-77443
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TYPE: DNA
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44 TATCATTTTTTTTTTTATTATTATTATTTTAAGTTTTTAGGGTACATGTGCAAAGTG 103
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Pred. No. 4.8e-12;
0; Mismatches 7;
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; Sequence 469, Application US/0998429
; Patent No. 7026447
; GENERAL INFORMATION:
    APPLICANT: Rosen et al.
    TITLE OF INVENTION: 53 Human Secreted Proteins
    TITLE OF INVENTION: 53 Human Secreted Proteins
    TITLE OF INVENTION: 53 Human Secreted Proteins
    CURRENT FILING DATE: 2001-10-30
    PRIOR APPLICATION NUMBER: 06/244,591
    PRIOR APPLICATION NUMBER: 06/244,591
    PRIOR FILING DATE: 1999-04-08
    PRIOR APPLICATION NUMBER: 60/661,463
    PRIOR APPLICATION NUMBER: 60/661,463
    PRIOR FILING DATE: 1997-10-09
    PRIOR APPLICATION NUMBER: 60/661,536
    PRIOR APPLICATION NUMBER: 60/661,536
    PRIOR PILING DATE: 1997-10-09
    PRIOR PILING DATE: 1997-10-09
FILE REFRENCE: PZ018P2
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT FILING DATE: 2000-10-30
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1997-00-08
PRIOR FILING DATE: 1997-10-09
PRIOR PRILING DATE: 1997-10-09
NUMBER: OF SEQ ID NOS: 727
SOCTWARRE: PALENTIN VEY: 2.0
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Best Local Similarity 94.1%;
Matches 111; Conservative
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TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
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7 ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; CURRENT APPLICATION NUMBER: US/09/949,016; CURRENT FILING DATE: 2000-04-14; PRIOR APPLICATION NUMBER: 60/241,755; PRIOR FILING DATE: 2000-10-20; PRIOR FILING DATE: 2000-10-03; PRIOR FILING DATE: 2000-10-03; PRIOR FILING DATE: 2000-09-08; NUMBER OF SEQ ID NOS: 207012; SOFFWARE: FASESEQ for Windows Version 4.0; SEQ ID NO 134975; LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                18893 TAAGTITITAGGGTACATGTGCACATTGTGCAGGTTAGTTACATATGTATACATGTGCCAT 18834
                                                                                                                                                                                                                                                                                                   78 AAGTITIAGGGTACAIGIGCAAAGIGIGCAGGITAGTIACAIAIAIATACAIGIGCCAIG 137
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                                                                                                                                                                                                                            18; Indels
                                                                                                                                                                                         DB 5;
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82.6%; Pred. No. 1.5e-11;
ive 0; Mismatches 25;
                                                                                                                                                                                     Score 104.2; DB 5
Pred. No. 1.6e-11;
                                                                                                                                                                                                                          0; Mismatches
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                                                                                        NAME/KEY: misc_feature

// LOCATION: (7234)...(7234)

// OTHER INFORMATION: n equals a,t,g, or C

US-09-984-429-469
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; Sequence 134975, Application US/09949016
; Patent No. 6812339
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; Patent No. 6812339
                                                                                                                                                                                       Query Match
Best Local Similarity 86.9%;
Matches 126; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 82.6
Matches 119; Conservative
               LENGTH: 42595
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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SEQ ID NO 469
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GENERAL INFORMATION:
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 15524
LIENGTARE: FSSLESC
LIENGTARE: LESSLESC
LIENGTARE: LES
APPLICATT: VENTER, J. Craig et al.

APPLICATT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR PAPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

SEQ ID NOS: 207012

SEQ ID NOS: 207012
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82.6%; Pred. No. 1.9e-11;
tive 0; Mismatches 25; Indels
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    LOCATION: (1)...(256171)
    CTHER INFORMATION: n = A,T,C or G
US-09-949-016-12822

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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15524
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82.6%;
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Best Local Similarity 82.6
Matches 119; Conservative
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NAME/KEY: misc feature
LOCATION: (1)...(25617:
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NAME/KEY: misc_feature
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Best Local Similarity
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Patent No. 6900016
GENERAL INFORMATION:
FACTOR OF 1 Craig et al.
FATTLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRICH FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 10823
SOUTHWARE: FastSEQ for Windows Version 4.0
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Patent No. 6900016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
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86.2%; Pred. No. 2.7e-11;
tive 0; Mismatches 19;
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13358
LENGTH: 260247
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Best Local Similarity 82.3%;
Matches 130; Conservative
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Matches 125, Conservative
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US-09-949-002-2044/c
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                                                                                                        TYPE: DNA
ORGANISM: Human
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LENGTH: 601
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FACULT NO. SULZASI
FACULTE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFRENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRICK APPLICATION NUMBER: 60/241,755
FRICK APPLICATION NUMBER: 60/241,756
FRICK APPLICATION NUMBER: 60/241,768
FRICK APPLICATION NUMBER: 60/231,768
FRICK FILING DATE: 2000-10-03
FRICK FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FREUESEQ for Windows Version 4.0
LENGTH: 86980
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Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PLICATION NUMBER: 60/241,755

PRIOR PAPLICATION NUMBER: 60/231,768

PRIOR PLILNG DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PLILNG DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498
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    Gaps
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0
    Indels
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Pred. No. 2e-11;
0; Mismatches 27;
    0; Mismatches
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; Sequence 15344, Application US/09949016
; Patent No. 6812339
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Best Local Similarity 81.6%;
Matches 120; Conservative
    Matches 119; Conservative
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Sequence 622, Application US/09949002
| Sequence 622, Application US/09949002
| Patent No. 6900016
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUE DISEASE, METHODS OF DETECTION
| TITLE OF INVENTION: AND USES THEREOF
| FILE REFERENCE: L0000790
| CURRENT APPLICATION NUMBER: US/09/949,002
| CURRENT FILING DATE: 2000-01-28
| PRIOR APPLICATION NUMBER: 60/231,401
| PRIOR APPLICATION NUMBER: 60/231,401
| PRIOR APPLICATION NUMBER: 108/23|
| SOFTWARE: FascSEQ for Windows Version 4.0
| SEQ ID NO 622
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86.2%; Pred. No. 3.2e-11;
tive 0; Mismatches 19;
GENERAL INFORMATION:
GENERAL INFORMATION:
1 TITLE ROSON CALL
1 TITLE OF INVENTION: 53 Human Secreted Proteins
1 TITLE OF INVENTION: 53 Human Secreted Proteins
1 TITLE OF INVENTION: 53 Human Secreted Proteins
1 TITLE OF INVENTION: 100 HUMBER: US/09/984,429
1 CURRENT FILING DATE: 2000-11-01
1 PRIOR APPLICATION NUMBER: 60/244,591
1 PRIOR APPLICATION NUMBER: 09/288,143
1 PRIOR FILING DATE: 1999-04-08
1 PRIOR APPLICATION NUMBER: 00/061,463
1 PRIOR APPLICATION NUMBER: 60/061,463
1 PRIOR APPLICATION NUMBER: 60/061,529
1 PRIOR FILING DATE: 1997-10-09
2 PRIOR FILING DATE: 1997-10-09
3 PRIOR FILING DATE: 1997-10-09
4 PRIOR PILING DATE: 1997-10-09
5 PRIOR APPLICATION NUMBER: 60/061,527
6 PRIOR APPLICATION NUMBER: 60/061,537
6 PRIOR PILING DATE: 1997-10-09
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Matches 125; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Human
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Patent No. 6900016
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
TITLE OF INVENTION: AND USES THERBOF
TITLE OF INVENTION: AND USES THERBOF
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/231,401
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSEQ for Windows Version 4.0
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                           FILE REFERENCE: CL000790
CURRENT APPLICATION NUMBER: US/09/949,002
CURRENT FILING DATE: 2000-01-28
FRIOR APPLICATION NUMBER: 60/231,401
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 10823
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2045
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         AND USES THEREOF
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US-09-984-429-448/c
; Sequence 448, Application US/09984429
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 86.2<sup>3</sup>
Matches 125; Conservative
         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Human
US-09-949-002-2045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-09-949-002-703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 18999
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1; Gaps

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Length 26225;

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PRIOR FILING DATE: 1998-10-08
PRIOR PPLICATION NUMBER: 60/061,463
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,529
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR PLING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,527
PRIOR APPLICATION NUMBER: 60/061,536
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
SEQ ID NO 309
SEQ ID NO 309
LENGTH. 21597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature; LCCATION: (1)...(194889); COTHER INFORMATION: n = A,T,C or G US-09-949-016-15654
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Best Local Similarity 77.6%;
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 94.6%;
Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-09-984-429-309
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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APPLICANT: UNEXPER, J. Craig et al.
APPLICANT: UNEXPER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRASESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 13173
LENGTH: 360470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273342 ITAAGITTTTAGGGTACATGTGCACAATGTGCCGGTTACTTACATATGTATATAATGTGCCA 273383
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                                1; Gaps
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                                Indels
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         86.2%; Pred. No. 3.2e-11;
tive 0; Mismatches 19;
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86.2%; Pred. No. 3.6e-11;
iive 0; Mismatches 19;
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Sequence 309, Application US/09984429

Patent No. 7026447

GENERAL INPORMATION:
TITLE OF INVORITION: 53 Human Secreted Proteins
TITLE OF INVORITION: 53 Human Secreted Proteins
TITLE OF INVORITION: 53 Human Secreted Proteins
TITLE OF INVORITION: 54 Human Secreted Proteins
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/288,143
PRIOR APPLICATION NUMBER: 09/288,143
PRIOR APPLICATION NUMBER: PCT/US98/21142
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                                                                                                                                                                                                                                                          137 GCTGGTGTGCTGCACCCATTAACTC 161
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         Best Local Similarity 86.2
Matches 125; Conservative
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Best Local Similarity 86.2
Matches 125; Conservative
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ORGANISM: Human
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US-09-949-016-15654

Sequence 15654, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VERTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOCTHARE: PESESEQ for Windows Version 4.0

LENGTH: 194889
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                                                                                                                50 TITCITITITITATIATIATATACTITITAAGTITITAGGGTACATGTGCAAAGTGTGCAGG
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                                                            Gaps
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Score 102.4; DB 5; Length 21597; Pred. No. 3.5e-11; 0; Mismatches 6; Indels 0;
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US-09-949-016-12415

US-09-949-016-12415

Sequence 12415, Application US/09949016

Sequence 12415, Application US/09949016

Patent No. 681239

TELE OF INVENTION: VOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION UNMER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12415

LENGTH: 353032
                                                                                                                                                                            Sequence 13367, Application US/09949016

Patent No. 6812339

GENERAL INPORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
SPRIOR FILING DATE: 2000-10-03
SPRIOR FILING DATE: 2000-10-03
SPRIOR FILING DATE: 2000-10-03
SOUTHARE: FASTESO FOR Windows Version 4.0
SEQ ID NO 13367
LENGTH: 69924
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                             153 CATTAACTC 161
                                                                         206 CATTAACTC 214
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NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15367
                                                                                                                                              RESULT 19
US-09-949-016-15367
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ORGANISM: Human
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                                                                                           107969 TAC-TITAAGTITITAGGGTACATGTGCACATTGTGCAGGTTAGTTACATATGTATACATG 108027
                                                                                                                                                                                                                                                                                      Sequence 18942, Application US/09513999C
; Sequence 18942, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dunas Milne Edwards, J.B.
; APPLICANT: Duclart, A.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT PILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER: OF SEQ ID NOS: 36681
; SEQ ID NO 18942
; LENGTH: 325
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; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-18942
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Best Local Similarity 83.71
Matches 108; Conservative
                                                                                                                                         190 CAGTTTTAGTCA 201
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: m=a
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LOCATION: 127
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LOCATION: 130
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US-09-513-999C-18942
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Query Match
Best Local Similarity 64.5%;
Matches 182; Conservative
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                                                                                                                                                                                                                                                                                    LENGTH: 181251
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Sequence 15754, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFRENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 363033
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                                                                              Query Match 14.4%; Score 101; DB 3; Length 363032; Best Local Similarity 79.9%; Pred. No. 7.3e-11; Matches 119; Conservative 0; Mismatches 30; Indels 0;
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Best Local Similarity 79.9%; Pred. No. 7.3e-11;
Matches 119; Conservative 0; Mismatches 30; Indels 0;
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Parent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
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NAME/KEY: misc_feature
LOCATION: (1)...(363033)
CTHER INFORMATION: n = A,T,C or G
US-09-949-016-15754
; LOCATION: (1)...(363032)
; OTHER INFORMATION: n = A,T,C or
US-09-949-016-12415
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RESULT 23
US-09-949-016-15091/c

1 Sequent No. 6812339

1 GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

1 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

1 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1 CURRENT APPLICATION NUMBER: US/09/949,016

1 CURRENT APPLICATION NUMBER: 60/241,755

1 PRIOR PILING DATE: 2000-10-20

2 PRIOR PILING DATE: 2000-10-03

3 PRIOR FILING DATE: 2000-10-03

4 PRIOR FILING DATE: 2000-09-08

5 NUMBER OF SEQ ID NOS: 207012

5 SOFTWARE: FastSEQ for Windows Version 4.0

5 SEQ ID NO 15091
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-00-08

NUMBER: 60/231,498

NUMBER: 60/230,000-00-08

NUMBER: FASTESEQ FOR Windows Version 4.0
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Pred. No. 7.8e-11;
0; Mismatches 97,
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Sequence 15703, Application US/09949016
; Sequence 15703, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; RIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15703
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Pred. No. 7.5e-11;
0; Mismatches 21;
                                                              APPLICANT: Rosen et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: PZ018P2
                                                                                                                                     FILE REFERENCE: FZOLBEYZ
CURRENT APPLICATION NUMBER: US/99/984,429
CURRENT FILING DATE: 2001-10-30
PRIOR FILING DATE: 2001-11-01
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR APPLICATION NUMBER: 06/061,463
PRIOR APPLICATION NUMBER: 06/061,463
PRIOR APPLICATION NUMBER: 60/061,463
PRIOR FILING DATE: 1997-10-09
PRIOR PRILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,536
PRIOR APPLICATION NUMBER: 60/061,536
PRIOR PRILING DATE: 1997-10-09
PRIOR PRILING DATE: 1997-10-09
PRIOR PRILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 727
SOFTWARE: PARCHININ VEY: 2.0
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Best Local Similarity 84.9%;
Matches 124; Conservative (
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ORGANISM: Homo sapiens
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ORGANISM: Human
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LENGTH: 1055
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                                                                 0; Gaps
Score 100.8; DB 3; Length 193169; Pred. No. 7.8e-11; 0; Mismatches 27; Indels 0;
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Fatent No. 7026447
GENERAL INFORMATION:
J. APPLICAUT: Rosen et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFRENCE: P2018P2
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT FILING DATE: 2001-10-30
FRIOR APPLICATION NUMBER: 09/244,591
FRIOR FILING DATE: 1999-04-08
FRIOR FILING DATE: 1999-10-08
FRIOR FILING DATE: 1998-10-08
FRIOR FILING DATE: 1998-10-08
FRIOR FILING DATE: 1999-10-09
FRIOR FILING DATE: 1997-10-09
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US-09-984-429-454/c
; Sequence 454, Application US/09984429
14.4%;
                               Best Local Similarity 81.2
Matches 117; Conservative
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US-09-984-429-426
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   Query Match
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FILE REFERENCE: CL001307
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ORGANISM: Human
                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
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Fatent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

FRIOR PILING DATE: 2000-10-20

FRIOR FILING DATE: 2000-10-02

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTMARE: FEASESEQ for Windows Version 4.0
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Sequence 150430, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

A PAPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND
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                                                                           1; Gaps
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14.3%; Score 100.4; DB 3; Length 144362;
Best Local Similarity 82.5%; Pred. No. 9.2e-11;
Matches 127; Conservative 0; Mismatches 26; Indels 1;
                               Length 91538;
                               Query Match
Best Local Similarity 84.9%; Pred. No. 9e-11;
Matches 124; Conservative 0; Mismatches 21; Indels
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                                                                                                                                                                                                                                                                                       136 TGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(144162)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                US-09-949-016-16066/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-949-016-16066
US-09-949-016-15703
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LENGTH: 144362
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Sequence 13420, Application US/09949016

| Sequence 13420, Application US/09949016
| Patent No. 681239
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| CURRENT APPLICATION NUMBER: 60/241,755
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR APPLICATION NUMBER: 60/237,768
| PRIOR APPLICATION NUMBER: 60/231,498
| PRIOR FILING DATE: 2000-10-03
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Best Local Similarity 81.5%; Pred. No. 9.6e-11;
Matches 128; Conservative 0; Mismatches 28; Indels
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FILE KEFERGER CONTRON NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 06/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
SOFTWARE: FELING DATE: 2000-10-06
SOFTWARE: FELING DATE: 2000-09-08
SEQ ID NO: 150430
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13420
LENGTH: 47363
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OTHER INFORMATION: n = A, T, C or G
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Matches 146; Conservative
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14.3%;
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86.0%;
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Best Local Similarity 89.3
Matches 108; Conservative
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LOCATION: (1)...(45039)
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Best Local Similarity
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    PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Human
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| Sequence 12611, Application US/09949016
| Patent No. 681239
| Patent No. 681239
| FARENEAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| FILE REFERENCE: CL001307
| CURRENT FILING DATE: 2000-04-14
| PRIOR PELICATION NUMBER: 60/241,755
| PRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-03
| PRIOR FILING DATE: 2000-09-08
| PRIOR FILING DATE: 2000-09-08
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BEREAL INFORMATION:
REPEARL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/237,768
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41 AAATATCATTTTCTTTTTTTTTATTATTATTTAAGTTTTTAGGGTACATGTGCAAA 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 100.2; DB 3; Length 135476;
Pred. No. 1e-10;
0; Mismatches 13; Indels 0; (
                                                                                                                                                 11692 TACATGTGCCATGCTGTGTGCTGCACCCATTAACTC 11728
                                                                                                                             TACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)....(135476)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12611
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Best Local Similarity 89.3%;
Matches 108; Conservative
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FACENTEAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REPERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949, 016

CURRENT PELLING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 15473
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                                                                                                                                                                                                                                                                                                               Score 100.2; DB 3; Length 135476;
Pred. No. 1e-10;
0; Mismatches 13; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 450395;
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Pred. No. 1.1e-10;
0; Mismatches 18
NUMBER OF SEQ ID NOS: 207012
SOFTWARER: FASTSEQ for Windows Version 4.0
SEQ ID NO 14413
LENGTH: 135476
TYPE: DNA
ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 15473, Application US/09949016; Patent No. 6812339
                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1)...(135476)
// OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14413
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15473
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TYPE: DNA
ORGANISM: Homo sapiens
US-09-245-041-16
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFREENCE: CL001307
CURRENT APPLICATION NUMBER: 00/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-20
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTHARE: PASESEC for Windows Version 4.0
SEQ ID NO 16065
                                                                                                                                         APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,758
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOCTHARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 13404
LENGTH: 237863
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Pred. No. 1.2e-10;
0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
14.3%; Score 100; DB 3; Length 237863;
Best Local Similarity 80.6%; Pred. No. 1.1e-10;
Matches 129; Conservative 0; Mismatches 30; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16065, Application US/09949016 Patent No. 6812339
                                                                                                   ; Sequence 13404, Application US/09949016; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 81.1%;
Matches 116; Conservative
321248 CATTAACTC 321256
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; ORGANISM: Human
US-09-949-016-13404
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US-09-949-016-16065
                                                                                   US-09-949-016-13404
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RESULT 36
US-09-358-055B-16/C
; Sequence 16, Application US/09358055B
; Patent No. 6713277
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Moste, D.L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TITLE OF INVENTION: TREATHENT OF BODY WEIGHT DISORDERS INCLUDING; TITLE OF INVENTION: OBESITY
; FILE REFERENCE: 7853-151
; CURRENT APPLICATION WUMBER: US/09/358,055B
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/245,041
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1.1e-10;
18 TTTTTTTTTGATGATTTTAATAAAATATCATTTTCTT
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14.2%; Score 99.6; Dl
Best Local Similarity 80.1%; Pred. No. 1.1e-
Matches 117; Conservative 0; Mismatches
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                                                                                                                                             125254 TTGGTATGCTGCACCCATTAACT 125232
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                                                                                                                            138 CTGGTGTGCTGCACCCATTAACT 160
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RESULT 39
US-09-949-016-14374/c
                                                                                                                                                            TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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US-09-949-016-13276/c
US-09-949-016-13276, Application US/09949016
; Sequence 13276, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                4006 Traagiririagggracargracaacargcaggrirgrracarargraracarargcca 3947
                                                                                                                                   4006 fraagrifiragggracargregacaacargcaggrificaracarargrafacarargcca 3947
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                                                                                                            Gaps
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0
                                                             Score 99.6; DB 3; Length 4072;
Pred. No. 1.1e-10;
0; Mismatches 29; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 4072;
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80.1%; Pred. No. 1.1e-10;
tive 0; Mismatches 29; Indels
                                                                                                                                                                                                                       3946 TGTTGGTGTGCTGCACCCATTAACTC 3921
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                                                          Query Match
Best Local Similarity 80.1%;
Matches 117; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.19
Matches 117; Conservative
           TYPE: DNA
CORGANISM: Homo sapiens
US-09-358-0558-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Homo sapiens
US-09-893-238-16
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LENGTH: 4072
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Sequence 14374, Application US/09949016

Batent No. 681239
GENERALI INCORMATION:
THE DEVELIANT OF USUARENTION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE PRACES FRACES for Windows Version 4.0
SEQ ID NO 14374
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Pred. No. 1.3e-10;
0; Mismatches 29; Indels 0;
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14.2%; Score 99.6; DB 3; Length 1
Best Local Similarity 83.3%; Pred. No. 1.3e-10;
Matches 125; Conservative 0; Mismatches 24; Indels
FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-03

PRIOR FILING DATE: 2000-09

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 13276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10261 TGCTGGTGCGCTGCACTAACTC 10236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)...(100877); OTHER INFORMATION: n = A,T,C or G US-09-949-016-13276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)...(112623)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 80.1%;
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
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Gaps

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4955 riririririadakoraakorriaaakororrirarrirarrirarrarrarrarkarkorr
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                                                                                                                                                                                                                                                                                              Length 7380;
                                                                                                                                                                                                                                                                                              14.2%; Score 99.4; DB 5; Length 7 84.8%; Pred. No. 1.3e-10; artive 0; Mismatches 21; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: PZ018P2
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/244,591
PRIOR FILING DATE: 1909-04-08
PRIOR PLING DATE: 1909-04-08
PRIOR PLING DATE: 1909-04-08
PRIOR PLING DATE: 1999-10-09
PRIOR APPLICATION NUMBER: 60/061,463
PRIOR PLING DATE: 1997-10-09
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PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION WUMBER: 60/061,532
PRIOR FILING DATE: 1997-10-09
NUMBER OF SEQ ID NOS: 727
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 455
LENGTH: 7380
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US-05-984-429-342/c
i, Sequence 342, Application US/09984429
i, Patent No. 7026447
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                                                                                                                                                                                                                                                                                                                                                      Matches 123; Conservative
                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-984-429-455
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Best Local Similarity
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Best Local Similarity
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     57037 ACT-TTAAGTTTTAGGGTACATGTGCACAATGTCCAGCTTAGTTACATATGTATATACATGT 56979
                                                          131
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                                                                                                                                                                                                                                                                                           RESULT 40

US-10-104-047-550

is Sequence 550, Application US/10104047

patent No. 6943241

general Information:
TICLE OF INVERTION:
TILE OF INVERTION: No. 6943241e1 full length cDNA
FILE REPERENCE: H1-A0105

CURRENT FILING DATE: 202-03-25

PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 ACATGTGCCATGCTGTGTGCTGCACCCATTAACTCA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 ACATGTGCCATGTTGGTTTGCTGCACCCATTAACTCA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: 53 Human Secreted Proteins
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFRENCE: P2018P2
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT APPLICATION NUMBER: 60/244,591
PRIOR APPLICATION NUMBER: 60/244,591
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-04-08
PRIOR FILING DATE: 1999-10-08
PRIOR PELLING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,529
                                                                                                                                                                                             56978 GCCATGCTGGTGTGCTGCACCATTAACTC 56949
                                                                                                                                                                    132 GCCATGCTGGTGTGCTGCACCCATTAACTC 161
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; Sequence 455, Application US/0984429
; Patcht NO. 7026447
; GENERAL INFORMATION:
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APPLICATION NUMBER: 60/061,527
FILING DATE: 1997-10-09
APPLICATION NUMBER: 60/061,536
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Matches 121, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
US-10-1047-550
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; NAME/KEY: misc_feature
; LCCATION: (1)...(116592)
; OTHER INFORMATION: n = A,T,C or G
US-10-354-065-3
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                         14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 82.4%;
Matches 126; Conservative
                       Query Match
Best Local Similarity 82.4
Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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US-09-949-016-12614/c
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                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT APPLICATION NUMBER: 00/241, 755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: BEASLEY, Ellen et al.
APPLICANT: BEASLEY, Ellen et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1192
CURRENT APPLICATION NUMBER: US/09/818,512
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
61
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14.2%; Score 99.4; DB 3; Length 64049;
Best Local Similarity 80.1%; Pred. No. 1.4e-10;
Matches 129; Conservative 0; Mismatches 31; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50443 GTATACATGTGCCATGCTGCTGCTGCACCCACTAACTCA 50483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15744
LENGTH: 64049
                                                                             Sequence 15744, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ...
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(116592)
COTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09818512
Patent No. 6537780
                                                                                                                                                 RESULT 43
US-09-949-016-15744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Human
US-09-949-016-15744
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LENGTH: 116592
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Sequence 12614, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: CLO01307
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR PAPLICATION NUMBER: 60/241,755
PRIOR PAPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: BEASLEY, Ellen et al.
APPLICANT: BEASLEY, Ellen et al.
TITLE OF INVENTION: ACID HUMAN ENZYME PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CLOOI192DIV
CURRENT APPLICANT NUMBER: US/10/354,065
CURRENT APPLICANT NUMBER: US/10/354,065
CURRENT FILING DATE: 2003-01-30
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 116592
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                                                  Gaps
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                                               1;
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Pred. No. 1.4e-10;
0; Mismatches 26; Indels 1;
Length 116592;
                                               26; Indels
Score 99.4; DB 3;
Pred. No. 1.4e-10;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                       48590 ACATGTGCCATGCTGGTGCGCTGCACCACTAA 48622
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                                                                                                                                                                                                                                                                              126 ACATGTGCCATGCTGGTGTGCTGCACCCATTAA 158
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Sequence 14577, Application US/09949016

Sequence 14577, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WIMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRAESEQ for Windows Version 4.0

SEQ ID NO 14577

LENGTH: 678533
                                                                                                                                               Sequence 13027, Application US/09949016
; Sequence 13027, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,756
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-00-03
; PRIOR FILING DATE: 2000-00-03
; RIOR FILING DATE: 2000-00-03
; RIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30410 GGTACATGTGCACATGTGCAGGTTAGTTACATATGTATACATGTGCCATGCTGGTGTGC 30351
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14.1%; Score 99; DB 3; Length 451:
Best Local Similarity 88.1%; Pred. No. 1.6e-10;
Matches 119; Conservative 0; Mismatches 15; Indels
                                 213809 TGTACTGCACCCATTAACTC 213790
  142 TGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ); NAME/KEY: misc_feature; LCCATION: (1)...(45138); OTHER INFORMATION: n = A,T,C or G US-09-949-016-13027
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                                                                                                                             RESULT 48
US-09-949-016-13027/c
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ORGANISM: Human
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US-09-949-016-14577
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USEQUENCE 16061, Application US/09949016

Sequence 16061, Application US/09949016

Sequence 16061, Application US/09949016

Sequence 16061, Application US/09949016

Sequence 16061, Application US/0949016

FILE REPERBALING NUMBER 10 (1)

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION NUMBER: US/09/949, 016

CURRENT APPLICATION NUMBER: US/09/949, 016

PRIOR APPLICATION NUMBER: 60/241, 755

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SSOFTWARE: FESTEREQ FOR Windows Version 4.0

LENGTH: 250958
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 TITITIGATGATTITAATAAATATCATTITITITITITITATTATTATACTTTTAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                         Query Match
14.2%; Score 99.2; DB 3; Length 248968;
Best Local Similarity 86.4%; Pred. No. 1.6e-10;
Matches 121; Conservative 0; Mismatches 18; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 250958;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
14.2%; Score 99.2; DB 3; Length 250
Best Local Similarity 86.4%; Pred. No. 1.6e-10;
Matches 121; Conservative 0; Mismatches 18; Indels
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION UNMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTERO for Windows Version 4.0
SEQ ID NO 12614
LENGTH: 248968
TYPE: DNA
TYPE: DNA
FEATURE:
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                                                                                                                                                                                                                                                NAME/KEY: misc_feature

| LOCATION: (1)...(248968)

| OTHER INFORMATION: n = A,T,C or G

US-09-949-016-1264
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CTHER INFORMATION: n = A,T,C or G
US-09-949-016-16061
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ORGANISM: Human
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GENERAL INFORMATION:
APPLICANT' EVENTER, VENTER, VENTE
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Sequence 59510, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PAPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR PAPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 2007012

SOFTWARE: FREESE OF WINDOWS Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.1%; Score 98.8; DB 3;
83.8%; Pred. No. 1.5e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 124; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Human
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ORGANISM: Human
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patence No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE OF INVENTION: WIMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 14578

LENTHARE: FRANKE: FRANKE: FRANKE: FRANKE: FRANKE: FRANKE: FRANKE: FRANKE: MUMBER: WIMBER: W
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                                                                                                                                                                                                                                                                                DB 3; Length 678533;
                                                                                                                                                                                                                                                                            Query Match
14.1%; Score 99; DB 3; Length 678
Best Local Similarity 82.8%; Pred. No. 1.8e-10;
Matches 125; Conservative 0; Mismatches 25; Indels
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                                                                                                                 ; LOCATION: (1)...(678533)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | FEATURE:
| NAME/KEY: misc feature
| LOCATION: (1)...(678533)
| OTHER INFORMATION: n = A,T,C or G
| US-09-949-016-14578
                                                                             NAME/KEY: misc feature
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        ORGANISM: Human
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ORGANISM: Human
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US-09-949-016-59509
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; Sequence 59509, Application US/09949016

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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
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Best Local Similarity 78.73
Matches 118; Conservative
                                                                                                                                                                                                                                                                                            Best Local Similarity 78.7
Matches 118; Conservative
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                                                                                                                                                                         , ORGANISM: Human
US-09-949-001-32
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US-09-949-001-38/c
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LENGTH: 66525
                                                                                                                   LENGTH: 66524
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                                                                                                                                                    TYPE: DNA
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Sequence 32, Application US/09949001
Patent No. 6825336
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF FILE REPERENCE: CLO00799
CURRENT APPLICATION UNDBER: US/09/949,001
CURRENT PILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/231,323
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                                                                                                                                                                                                                                                                             Sequence 360, Application US/09984429
Fatent No. 702647
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: PZ018P2
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT FILING DATE: 2001-10-30
FRIOR APPLICATION NUMBER: 09/288,143
FRIOR FILING DATE: 1099-10-10
FRIOR PILING DATE: 1999-10-08
FRIOR FILING DATE: 1999-10-08
FRIOR FILING DATE: 1999-10-09
FRIOR FILING DATE: 1999-10-09
FRIOR PRICATION NUMBER: 60/061,529
FRIOR PAPLICATION NUMBER: 60/061,529
FRIOR PAPLICATION NUMBER: 60/061,529
FRIOR PAPLICATION NUMBER: 60/061,539
FRIOR APPLICATION NUMBER: 60/061,537
FRIOR FILING DATE: 1997-10-09
FRIOR FILING DATE: 1997-10-09
FRIOR FILING DATE: 1997-10-09
FRIOR FILING DATE: 1997-10-09
FRIOR APPLICATION NUMBER: 60/061,532
FRIOR APPLICATION NUMBER: 60/061,532
FRIOR FILING DATE: 1997-10-09
FRIOR APPLICATION NUMBER: 60/061,532
FRIOR FILING DATE: 1997-10-09
                                                                                                                            135 ATGCTGGTGTGCTGCACCCATTAACTCA 162
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Matches 123; Conservative
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US-09-984-429-360/c
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Sequence 13828, Application US/09949016
Factor No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 38, Application US/09949001
Patent No. 6825336
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH OSTEOPOROSIS, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,001
CURRENT PILING DATE: 2003-01-15
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 848
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                18218 ATACTITIAAGTITITIAGGGTACATGTGCAATGTGCAGGTTAGTTACATATGTACACATG 18159
                                                                                                                                                                                                            71 TACTITIAAGITITIAGGGTACAIGIGCAAAGIGTGCAGGITAGITACATATATATACATG 130
                                                                                                       71 TACTITITAAGITTTTAGGGTACATGTGCAAAGIGTGCAGGTTAGTTACATATATACATG
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  Length 66524;
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                                                   Indels
14.1%; Score 98.8; DB 3; 78.7%; Pred. No. 1.8e-10; tive 0; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                 131 TGCCATGCTGGTGTGCTGCACCCATTAACT 160
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Sequence 13730, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION: Craig et al.

FITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR PPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

NUMBER OF SEQ ID NOS: 207012

SEQ ID NOS: 207012

SEQ ID NOS: 207012
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISNS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

WHEN APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498
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          104954 TGTTGGTGCTGCACCCATTAACTC 104979
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; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       i LOCATION: (1)...(163181)
i OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13730
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NAME/KEY: misc_feature
LOCATION: (1)...(16318
                                                                                                                                              US-09-949-016-13730/c
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ORGANISM: Human
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LENGTH: 192700
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Sequence 1542, Application US/09880107

Batent No. 6974667

APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Scherf, Uwe

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERENCE: 4921-5028-W0

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT APPLICATION NUMBER: US 60/211,379

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR PLING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR SELING DATE: 2000-010-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE PARENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 87323;
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US-09-880-107-1542
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14.1%; Score 98.8; DB 3;
Best Local Similarity 78.7%; Pred. No. 1.8e-10;
Matches 118; Conservative 0; Mismatches 32;
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PASSEQ for Windows Version 4.0
SSOFTWARE: PASSEQ for Windows Version 4.0
LENGTH: 87323
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13828
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LENGTH: 110096
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FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                               TYPE: DNA
ORGANISM: Human
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US-09-949-016-13477
                                                                                                                          SEQ ID NO 15419
LENGTH: 212449
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Sequence 1718.2. Application US/09949016

Patent No. 681239

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOOL3137

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-03

SOCTHARE: FAST ED NOS: 207012

SOCTHARE: FAST EQ for Windows Version 4.0

SEQ ID NO 17182

LENTH: 192704
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Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION UNMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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84.2%; Pred. No. 1.9e-10;
ive 0; Mismatches 22; Indels 1;
                                Query Match 14.1%; Score 98.8; DB 3; Length 192700; Best Local Similarity 84.2%; Pred. No. 1.9e-10; Matches 123; Conservative 0; Mismatches 22; Indels 1;
                                                                                                                                                                                                                                                                                132359 TGCTGGTGCACTGCACCACTAACTC 132334
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Matches 123; Conservative
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US-09-949-016-17182/c
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US-09-949-016-15419
US-09-949-016-11820
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US-09-949-016-13477

Sequence 13477, Application US/09949016

Sequence 13477, Application US/09949016

Sequence 13477, Application US/09949016

Patent No. 6812339

CERRAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/291,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-0-10-03

SPRIOR PILING DATE: 2000-10-03

SPRIOR PILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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84.2%; Pred. No. 1.9e-10;
tive 0; Mismatches 22;
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Pred. No. 1.9e-10;
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15419
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Best Local Similarity 83.8<sup>3</sup>
Matches 124; Conservative
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Best Local Similarity 84.2<sup>3</sup>
Matches 123, Conservative
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Gaps

Length 146401;

DB 3;

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Score 98.6; DB 3; Length 1 Pred. No. 2e-10; 0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           137 GCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                               14.1%;
80.0%;
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Best Local Similarity 83.1%;
Matches 123; Conservative
                                                                                                            Query Match
Best Local Similarity 80.0
Matches 116; Conservative
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  ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16151
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-949-016-59511
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; Sequence 16151, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; FAPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR PILING DATE: 2000-10-20
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTHARE: FeatSEQ for Windows Version 4.0
; SEQ ID NO 16151
; LENGTH: 146401
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14.1%; Score 98.6; DB 5;
Best Local Similarity 92.0%; Pred. No. 1.8e-10;
Matches 104; Conservative 0; Mismatches 9;
                                                                                                                       Sequence 388, Application US/0984429

Patent No. 7026447

GENERAL INFORMATION:

APPLICATT: Rosen et al.

TITLE OF INVENTION: 53 Human Secreted Proteins

FILE REFERENCE: P2018P2

CURRENT APPLICATION NUMBER: US/09/984,429

CURRENT FILING DATE: 2001-10-30

PRIOR APPLICATION NUMBER: 60/244,591

PRIOR APPLICATION NUMBER: 09/288,143

PRIOR FILING DATE: 1999-04-08

PRIOR FILING DATE: 1999-04-08

PRIOR FILING DATE: 1999-10-09

PRIOR FILING DATE: 1997-10-09

PRIOR APPLICATION NUMBER: 60/061,463

PRIOR FILING DATE: 1997-10-09

PRIOR FILING DATE: 1997-10-09

PRIOR FILING DATE: 1997-10-09

PRIOR APPLICATION NUMBER: 60/061,529

PRIOR APPLICATION NUMBER: 60/061,529

PRIOR APPLICATION NUMBER: 60/061,536

PRIOR FILING DATE: 1997-10-09

PRIOR PRIOR FILING DATE: 1997-10-09

PRIOR PRIOR FILING DATE: 1997-10-09

PRIOR PRIOR FILING DATE: 1997-10-09
83021 ATGCTGGTGCGCTGCACCCACTAACTCA 83048
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ORGANISM: Homo sapiens
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                                                                             RESULT 63
US-09-984-429-398/c
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Sequence 59511, Application US/09949016
; Sequence 59511, Application US/09949016
; Batent No. 6812339
; GENERAL INFORMATION:
; APPLICAMT: VENTER, US. Craig et al.
; APPLICAMT: VENTER, US. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REPREEMENCE: CLOON 307
; CURRENT APLICATION NUMBER: 60/241, 755
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEC ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59511
Sequence 179319, Application US/09949016
Sequence 179319, Application US/09949016
Batent No. 681239
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
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                                                                                                                                 141748 GCTGGTGCGCTGCACTAACTC 141724
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3897 ITTTATTTTTTATTTTTTTTTTTTTATTATTATTATTATCAC-TTTAAGGTTTTTAGGGTACA 3839
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US-09-949-016-16065
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US-09-949-016-16065
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US-09-949-016-13675
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14.1%; Score 98.4; DB 5; Length 6407;
Best Local Similarity 90.6%; Pred. No. 2e-10;
Matches 116; Conservative 0; Mismatches 11; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 98.4; DB 3; Length 601;
Pred. No. 1.8e-10;
0; Mismatches 31; Indels
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1TILE OF INVENTION:
CURRENT ROSEN et al.
1TILE REFERENCE: PZ018P2
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT APPLICATION NUMBER: US/09/984,429
CURRENT FILING DATE: 2001-10-30
PRIOR PILING DATE: 1999-04-08
PRIOR PILING DATE: 1999-04-08
PRIOR PILING DATE: 1999-04-08
PRIOR PILING DATE: 1999-04-08
PRIOR PILING DATE: 1999-10-08
PRIOR PILING DATE: 1997-10-09
US-09-984-429-468/c
; Sequence 468, Application US/09984429
; Patent No. 7026447
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 IGTTICACATAAAGITTITTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.1%;
80.0%;
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Best Local Similarity 80.05
Matches 128; Conservative
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ORGANISM: Homo sapiens
US-09-984-429-468
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ORGANISM: Human
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Sequence 13675, Application US/09949016

patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASLSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                        Sequence 16065, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFREENCE: CLOU01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESTERQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 TGTGCAAAGTGTGCAGGTTAGTTACATATATATACATGTGCCATGCTGGTGTGCTGCACC 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 14.1%; Score 98.4; DB 3; Length 212139; Best Local Similarity 82.2%; Pred. No. 2.3e-10; Matches 125; Conservative 0; Mismatches 26; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89935 GTGCCATGCTGGTGCACTGCACCACTAACTC 89966
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                                                                                                                          153 CATTAACT 160
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THE SHEET STRING STRING
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Patent No. 6812339
GENERAL INFORMATION:
PAPELICANT: USANTION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WINDER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 12386
LENGTH: 263693
                                                                                                                                                                                                                                                                                                                            96649 Tririrgrirriciriricirircirrirarcciarianescaarricirrccirrira 96590
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                                                                                                                                                                                                                                                           1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                   Length 235452;
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14.1%; Score 98.4; DB 3; Length 26:
Best Local Similarity 80.0%; Pred. No. 2.3e-10;
Matches 128; Conservative 0; Mismatches 31; Indels
                                                                                                                                                                                                             Query Match 14.1%; Score 98.4; DB 3; Length 23: Best Local Similarity 84.7%; Pred. No. 2.3e-10; Matches 122; Conservative 0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96530 GTATACATGTGCCATGCTGGTGCTGCTGCACCCAGTAACTC 96491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96697 TTGGTGTGCTGCACCCATTAACTC 96720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 CTGGTGTGCTGCACCCATTAACTC 161
                                                                                | FEATURE:
| NAME/KEY: misc_feature
| LOCATION: (1)...(235452)
| OTHER INFORMATION: n = A,T,C or G
| US-09-949-016-13675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 70
US-09-949-016-12386/c
                                            TYPE: DNA
ORGANISM: Human
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SEQ ID NO 13675
LENGTH: 235452
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Search completed: July 19, 2006, 07:08:40 Job time : 204 secs

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Sequence 267264, Sequence 267264, Sequence 267265, Sequence 235941, Sequence 235941, Sequence 235941, Sequence 235943, Sequence 235943, Sequence 235943, Sequence 235943, Sequence 214, Appl Sequence 219, Appl Sequence 219, Appl Sequence 21353, Appl Sequence 21353, Appl Sequence 21253, Appl Sequence 21253, Appl Sequence 21253, Appl Sequence 21253, Appl Sequence 661, Appl Sequence 570607, Sequence 570607,

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Sequence 1, Application US/10661966
; Publication No. US20050277118A1
; GENERAL INFORMATION:
; APPLICANT: Noth, Richard B.
; APPLICANT: Noth, Richard B.
; APPLICANT: Nathew Roberts
; TITLE OF INVENTION: MATHORS FOR IDENTIFYING SUBJECTS AT RIS);
; TITLE OF INVENTION: OF MELANOWA AND TREATMENTS THEREOF
; FILE REFERENCE: 524592003800
; CURRENT APPLICATION NUMBER: US/10/661,966
; CURRENT PILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: 60410,595
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2 US-10-301-480-578850
2 US-10-301-480-1192559
5 US-10-301-480-1192559
1 US-10-322-281-214
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0 US-10-719-993-6940
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US-09-984-429-469
US-10-981-429-469
US-10-087-192-238
2 US-11-121-086-98
2 US-10-517-905-19
US-10-087-192-1330
US-10-741-600-17645
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2 US-10-301-480-577167

2 US-10-301-480-1190576

US-09-949-654-3

US-09-949-651-12101

US-09-764-80-661

US-10-074-805-661

US-10-212-872-661
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US-10-301-480-570607
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US-10-301-480-1166170
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US-10-027-632-256998
US-10-027-632-2569997
US-10-027-632-256998
US-10-301-480-91798
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US-10-301-480-705208
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US-09-764-869-1276
US-09-984-429-448
US-10-091-504-1276
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Sequence 6776, Ap
Sequence 6776, Ap
Sequence 267263,
Sequence 728921,
Sequence 728921,
Sequence 728921,
Sequence 354, App
Sequence 359, App
Sequence 27, Appl
Sequence 207, Appl
                                                                                                                     July 19, 2006, 07:08:31; Search time 1464 Seconds (without alignments) 5875.235 Million cell updates/sec
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                                                                                                                                                                                                                                   1 ctgtttcacataaagttttt.....gccttttaggtgatgtggca 700
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               GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-779-993-6776
US-10-027-632-267263
US-10-027-632-267263
US-09-925-065A-728921
US-09-984-429-354
US-10-311-455-369
US-10-221-714A-27
US-10-311-455-369
US-10-221-714A-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 70 summaries
                                                                                        - nucleic search, using sw model
                                                                                                                                                                                                                                                                       IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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No
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Sequence 256997, Sequence 25698, Sequence 256998, Sequence 91798, A Sequence 91799, A Sequence 705207, Sequence 705207, Sequence 1276, Ap Sequence 448, App Sequence 148, App

ALIGNMENTS

RISK

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ORGANISM: Homo
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US-10-719-993-6776
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LENGTH: 100364
                                                                                                       US-09-764-891-8028
                                                             LENGTH: 19167
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                                                                           TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146421 TAATTGATTTTACCAAATTTCCATGGAACAAACAAGGTTGGCTATTTTTTGGATTGATAT 146480
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                                                                                                                                                                                                                                146121 TATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTCACATGAAGTTTTTTTAAA 146180
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                                                                                                                                                                                                               Gaps
                                                                                                                                                     Length 190276;
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Publication No. US20030077808A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC006
CURRENT APPLICANT NUMBER: US/09/764,891
CURRENT PILING DATE: 2001-01-17
                                                                                                                                                                                 Indels
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Pred. No. 4.5e-118;
1; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/422,344
PRIOR FILING DATE: 2002-10-29
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                   100.0%;
99.9%; F
                                                                                                                                                                 Best Local Similarity 99.9
Matches 699; Conservative
                                                                                                       ORGANISM: Homo sapiens
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US-09-764-891-8028/c
                                                                           LENGTH: 190276
                                                                                                                     US-10-661-966-1
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LOCATION: (1). .. (100364)
COTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-7
US-10-719-993-6776
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                            30885
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US-10-027-632-267263/C
US-10-027-632-267263/C
; Sequence 267263, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 109.2; DB 9; Length 100364;
Pred. No. 1.4e-09;
0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                            Score 113.2; DB 3; Length 19167; Pred. No. 1.5e-10; 0; Mismatches 28; Indels 0;
- consult PALM or file wrapper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 ATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
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CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55542
SOFTWARE: PASKEEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6776, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
Prior application data removed
NUMBER OF SEQ ID NOS: 10231
SOFFWARE: PatentIn Ver. 2.0
SEQ ID NO 8028
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Best Local Similarity 84.2%;
Matches 123; Conservative
                                                                                                                                                                                                                            Query Match
Best Local Similarity 82.3%;
Matches 130; Conservative
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ORGANISM: Homo sapiens
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Gaps

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279 AIGCTATCCCCCCCTTATTAAATATTCTTATGTCATAAATATATTATTATAAAAGT 220
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GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Wang, David G. TITLE OF INVENTION: Udentification and Mapping of Single; ITTLE OF INVENTION: Udentification and Mapping of Single; ITTLE OF INVENTION: Udentification and Mapping of Single; ITTLE OF INVENTION: UNDER: US 60/925,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2001-01-16

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 107; DB 7;
Pred. No. 6.5e-10;
1; Mismatches 91;
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 267263
LENGTH: 563
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Best Local Similarity 65.8
Matches 185; Conservative
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Matches 122; Conservative
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-267263
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Dolymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/18,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
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Pred. No. 6.5e-10;
1; Mismatches 91; Indels
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     Polymorphisms in the Human Genome
                         FILE REFERENCE: 108827,129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US/10/027,632
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 1000-03-29
PRIOR FILING DATE: 1000-03-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEC ID NOS: 325720
SEC ID NO 267263
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Publication No. US20030204075A9
GENERAL INFORMATION:
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PRIOR PAPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION UNMBER: US 60/156,358
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Best Local Similarity 65.8
Matches 185; Conservative
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; ORGANISM: Human
US-10-027-632-267263
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ORGANISM: Homo sapiens
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GENERAL INFORMILLOW:
GENERAL INFORMILLOW:
GENERAL INFORMILLOW:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108627.135
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PELING DATE: 2000-10-24
PRIOR PELING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PELING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2001-10-16
PRIOR FILING DATE: 2001-10-16
PRIOR PELING DATE: 2001-01-16
SPRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-01-16
SPRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.3%; Score 107; DB 5; Length 596; 83.0%; Pred. No. 6.6e-10; ive 0; Mismatches 25; Indels
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Sequence 354, Application US/09984429

Publication No. US20040010132A1

GENERAL INPORMATION:

APPLICANT: Rosen et al.

TILLE OF INVENTION: 53 Human Secreted Proteins

FILE REPRENCE: PZ018P2

CURRENT APPLICATION NUMBER: US/09/984,429

CURRENT FILING DATE: 2001-10-30

PRIOR FILING DATE: 2000-11-01

PRIOR APPLICATION NUMBER: 09/244,591

PRIOR APPLICATION NUMBER: 09/288,143

PRIOR APPLICATION NUMBER: PCT/US98/21142

PRIOR APPLICATION NUMBER: PCT/US98/21142

PRIOR APPLICATION NUMBER: 60/61,463

PRIOR FILING DATE: 1999-00-08

PRIOR FILING DATE: 1999-10-08
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                                                                                                                      445 ATGCTGGTGCTGCACCCATTAACTC 471
                                                                                                                                                                                                                                                       Sequence 728921, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
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Matches 122; Conservative
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US-09-925-065A-728921
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Sequence 369, Application US/10311455
; Sequence 369, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
    APPLICANT: PIEPENBROCK, Christian
    APPLICANT: PIEPENBROCK, Christian
; APPLICANT: Diagnosis of Diseases Associated with the Immune System by Determi;
    TITLE OF INVENTION: Cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2001-0702
; PRIOR PILING DATE: 2001-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR PILING DATE: 2000-09-01
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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0; Mismatches 7;
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Pred. No. 1.7
PRIOR APPLICATION NUMBER: 60/061,529
PRIOR FILING DATE: 1997-10-09
PRIOR PLING DATE: 1997-10-09
PRIOR PLING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,527
PRIOR APPLICATION NUMBER: 60/061,527
PRIOR APPLICATION NUMBER: 60/061,536
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
PRIOR PILING DATE: 1997-10-09
SPRIOR PILING DATE: 1997-10-09
SPRIOR PILING DATE: 1997-10-09
SEQ ID NO 354
LENGTH: 9766
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ORGANISM: Artificial Sequence
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Best Local Similarity 94.1%;
Matches 111; Conservative
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APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: DIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
TITLE OF INVENTION: Method and nucleic acids for the analysis of astrocytomas
FILE REFERENCE: 5013.1013
CURRENT APPLICATION NUMBER: US/10/311,507
CURRENT FILING DATE: 2002-12-16
PRIOR PELING DATE: 2001-07-02
PRIOR PELING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PELING DATE: 2000-06-30
PRIOR PELING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 136
SEQ ID NO 95
LENGTH: 8666
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        ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-507-95
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US-10-311-507-95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: PIEPENBROCK, Christian
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: Lumor Suppressor genes and oncogenes
FILE REPERENCE: 5013.1005
CURRENT APPLICATION NUMBER: US/10/221,714A
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: DE 10013847.0
PRIOR FILING DATE: 2000-03-15
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 540

SEQ ID NO 27

LENGTH: 8666
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US-09-925-065A-477191/c
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LENGTH: 493
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                                                                                                                                                                                                                                                                                          TAACTACTCTGATAAAAAGTTTTATAGTTTCCTACTTTTAAGCAAAATTCCATAGGGCA 311
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; Sequence 207, Application US/10433793
; Publication No. US20040142334A1
; GENERAL INFORMATION:
    APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von mit Angiogenese assoziierten Krankheiten
; FILE REFERENCE:
    CURRENT APPLICATION NUMBER: US/10/433,793
; CURRENT FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 212
; SEQ ID NO 207
: LENGTH: 8666
                                               372 TAAGTATAATTTAATATTGTCAAATAATTTGGAAAATACCATGGGTACTTAATTGATTTT
                                                                                                           72 ACTITITAAGITITIAGGGTACATGIGCAAAGIGIGCAGGITAGITACATATATACATGI
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   Pred. No. 1.9e-09;
0; Mismatches 324; Indels
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ORGANISM: Artificial Sequence
FEATURE:
    49.08;
                 Matches 312; Conservative
   Best Local Similarity
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1906 İTTAİAATGİAİTTAAAİGİTGTTİTTAİATĞGTTGİATTTİTTAİTTİTTIAAİA 1965
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372 TAAGTATAATTTAATATTGTCAAATAATTTGGAAAATACCATGGGTACTTAATTGATTTT
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-30
PRIOR PILING DATE: 2000-11-6
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PILING DATE: 2001-01-6
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-6
PRIOR PILING DATE: 2001-01-6
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252 TAACTACTCTGATAAAAAGTTTTATAGTTTCCTACTTTTA 292
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US-10-027-632-267266
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GENERAL INFORMATION:
JULIANT: WANG; David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR PAPLICATION NUMBER: US 60/243,096
PRIOR PELING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PELING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PELING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FRASESQ for Windows Version 4.0
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le-09;
-haq 92; Indels
                                                              12 AAAGTTTTTTTTTTTGATGATTTTAATAAAATATCATTTTCTTTTTT
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                          0; Mismatches
          Pred. No.
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      65.8%;
                          Matches 185; Conservative
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CORGANISM: Homo sapiens
US-09-925-065A-477191
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Best Local Similarity
        Best Local Similarity
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AC-TTTAAGTTTTAGGGTACATGTGCACAATGTGCAGTTTAGTTACATATGTATATATCTTT 272
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                                                                                                                  Gaps
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Publication No. US20030204075A9
GENERAL INFORMATION:
APPLICATION MANG, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.128
CURRENT APPLICATION NUMBER: US/10/027,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 498;
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Pred. No. 1e-09;
0; Mismatches 92; Indels
149 TITCCIGITIAAAATGTATTATTCAATGGTTTAGTGTTTTA 109
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                                                                            , Sequence 267266, Application US/10027632; Publication No. US20020198371A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.1%;
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Best Local Similarity 65.8
Matches 185; Conservative
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Sequence 267262, Application US/10027632

Publication No. US200304075A9

GENERAL INFORMATION:

APPLICANT' Wang, David G.

TITLE OF INVENTION: Telemification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION WUMBER: US/10/027, 632

CURRENT APPLICATION NUMBER: US 60/128,006

PRIOR FILING DATE: 2002-04-30

PRIOR PELING DATE: 2000-00-129

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-03-24

PRIOR APPLICATION NUMBER: US 60/195,218

PRIOR PRILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-08-09

PRIOR PILING DATE: 1999-08-09
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Pred. No. 1.1e-09;
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Pred. No. 1.1e-09;
0; Mismatches 92
                                                                                                                                                                                                                                                                         0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 267262
LENGTH: 563
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 267262
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65.8%;
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Best Local Similarity 65.83
Matches 185; Conservative
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Best Local Similarity 65.8
Matches 185; Conservative
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US-10-027-632-267262
                                                                                                               TYPE: DNA
ORGANISM: Human
                                                                                        LENGTH: 563
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PRIOR FILING DATE: 2002-0198371A1

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

FITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108627.129

CURRENT FILING DATE: 2002-04-30

FRIOR PELING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-04-30

PRIOR FILING DATE: 2000-04-30

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-89

PRIOR FILING DATE: 1999-09-89
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0; Mismatches
                      PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-3
PRIOR FILING DATE: 1999-09-3
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PRIOR FILING DATE: 1999-09-3
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PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
PRIOR FILING DATE: 1999-09-09
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PRIOR PRIOR DATE: 1999-09-09
PRIOR PRIOR DATE: 1999-09-09
PRIOR PRIOR DATE: 1999-09-09
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Matches 185; Conservative
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Gaps

4,

Length 563;

7

4; Gaps

Length

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279 ATGCTATCCCCCCCTTATTAAATATTCTTATGTCATAAATATTATTATAAAATGT 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.1%; Score 105.4; DB 6; Length 563;
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                                                                                                                                                                                                                                                                                                                                                      Score 105.4; DB 6;
Pred. No. 1.3e-09;
1; Mismatches 92;
                  PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 563
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 267265
LENGTH: 563
APPLICATION NUMBER: US 60/167,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 267265, Application US/10027632 Publication No. US20020198371A1 GENERAL INFORMATION:
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Best Local Similarity 65.5%;
Matches 184; Conservative
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US-10-027-632-267265
                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
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                            131
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US-10-027-632-267264/c

$ sequence 267264, Application US/10027632

$ sequence 267264, Application US/10027632

$ publication No. US20020198371A1

$ GENERAL INFORMATION:

$ TILLE OF INVENTION: Identification and Mapping of Single Nucleotide

$ TILLE OF INVENTION: Polymorphisms in the Human Genome

$ TILLE OF INVENTION: Polymorphisms in the Human Genome

$ TILLE OF INVENTION: Polymorphisms in the Human Genome

$ TILLE OF INVENTION: Polymorphisms in the Human Genome

$ TILLE OF INVENTION: Polymorphisms in the Human Genome

$ TILLE OF INVENTION: Polymorphisms in the Human Genome

$ TILLE OF INVENTION NUMBER: US 60/218,006

$ PRIOR APPLICATION NUMBER: US 60/198,676

$ PRIOR PILING DATE: 2000-04-20

$ PRIOR PILING DATE: 2000-04-20

$ PRIOR PILING DATE: 2000-04-20

$ PRIOR PILING DATE: 2000-03-29

$ PRIOR FILING DATE: 2000-03-29

$ PRIOR FILING DATE: 2000-03-29

$ PRIOR FILING DATE: 2000-02-24
                       ACTITITAAGIITITAGGGTACATGTGCAAAGTGTGCAGGTTAGTTACATATATACATGT
                                                    395 AC-TTTAAGTTTTTAGGTACATGTGCACAATGTGCAGTTTAGTTACATGTACATGT
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Sequence 4, Application US/10304113

Sequence 4, Application US/10304113

PUBLICATION NO. US20040102623A1

GENERAL INFORMATION:
APPLICANT: Brett P. Monia

APPLICANT: Kenneth W. Dobie

TITLE OF INVENTION: MODULATION OF PAKI EXPRESSION
FILE REFERENCE: RTS-0415

CURRENT APPLICATION NUMBER: US/10/304,113

CURRENT FILING DATE: 2002-11-23

NUMBER OF SEQ ID NOS: 167

LENGTH: 70043
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Best Local Similarity
Matches 126; Conserva
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ORGANISM: H. sapiens
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Gaps

4

92; Indels

Length 563;

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APPLICANT: Wang, David G.

ITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITLE OF INVENTION: Identification in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR FILING DATE: 2000-07-12
FRIOR FILING DATE: 2000-04-20
FRIOR PAPLICATION NUMBER: US 60/198,676
FRIOR FILING DATE: 2000-03-29
FRIOR PAPLICATION NUMBER: US 60/195,218
FRIOR PAPLICATION NUMBER: US 60/165,363
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR APPLICATION NUMBER: US 60/157,363
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR APPLICATION NUMBER: US 60/166,002
FRIOR APPLICATION NUMBER: US 60/166,002
FRIOR APPLICATION NUMBER: US 60/166,002
FRIOR APPLICATION NUMBER: US 60/166,002
FRIOR APPLICATION NUMBER: US 60/166,002
FRIOR APPLICATION NUMBER: US 60/166,002
FRIOR APPLICATION NUMBER: US 60/166,002
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192 GTTTTAGTCATTTTCCTAATTGAAAGTATCATAAGTAATCCATAAATTTTGAAAAAATGT 251
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                                                                       279 Argerarecerecececerrafraaararrecraarararararararararararara
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
File Reference: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/18,006
REIOR APPLICATION NUMBER: US 60/18,006
REIOR PILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/166,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
                           192 GITTTAGICATTTTCCTAATTGAAAGTATCATAAGTAATCCATAAATTTGAAAAAATGT
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                                                                                                                                252 TAACTACTCTGATAAAAAGTTTTATAGTTTCCTACTTTTA 292
                                                                                                                                                                                 219 Trrccrgrrraaargrarrarrcaarggrrragrgrrrra 179
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 267265
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Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
                                                                                                                                                                                                                                                                                                            Sequence 267265, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
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Best Local Similarity 65.5%;
Matches 184; Conservative
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US-10-027-632-235941/c
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                                                                                                                                                                                                               US-110-U2/10-264, Application US/10027632

Publication No. US20030204075A9

Publication No. US20030204075A9

Publication No. US20030204075A9

Publication No. US20030204075A9

FURDEMENT INFORMATION:

PUBLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-09-29

PRIOR FILING DATE: 2000-09-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-02-24

PRIOR PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-10-24

PRIOR PRIOR FILING DATE: 1999-10-24

PRIOR PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-08-09

PRIOR FILING DATE: 1999-09-08-09

PRIOR FILING DATE: 1999-09-08-09

PRIOR FILING DATE: 1999-09-08-09

PRIOR FILING DATE: 1999-09-08-09

PRIOR APPLICATION NUMBER: US 60/146,002

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PRIOR PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002
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Pred. No. 1.3e-09;
1; Mismatches 92;
Pred. No. 1.3e-09;
                                                   1; Mismatches
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Best Local Similarity 65.5%;
Matches 184; Conservative
                              65.5%;
                           Best Local Similarity 65.5
Matches 184; Conservative
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US-10-027-632-267264
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337

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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 235942
LENGTH: 600
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Best Local Similarity 72.9%;
Matches 148; Conservative
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                                                                                                            ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235942
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ORGANISM: Human
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REPERBURE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR PELLOR DATE: 2000-07-12
FRIOR PELLOR DATE: 2000-07-12
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR FILING DATE: 2000-07-20
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR APPLICATION NUMBER: US 60/185,218
FRIOR APPLICATION NUMBER: US 60/185,218
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR PILING DATE: 1999-10-23
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
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Publication No. US20020198371A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/028,676
PRIOR FILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-24
PRIOR FILING DATE: 2000-04-24
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-11-23
PRIOR PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PRIOR DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-109-28
PRIOR PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PRIOR APPLICATION NUMBER: US 60/146,002
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Pred. No. 1.3e-09;
2; Mismatches 48;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 235941
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72.9%;
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Best Local Similarity 72.99
Matches 148; Conservative
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ORGANISM: Human
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118 ATATATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTCACATGAAGTTTTTTT 177
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| JENERAL INCRMANION:
| JENERAL INCRMANION: | David G. |
| TITLE OF INVENTION: | TODAMICA |
| TITLE OF INVENTION: | TODAMICA |
| TITLE OF INVENTION: | TODAMICA |
| FILE REFERENCE: 108827.129 |
| CURRENT APPLICATION NUMBER: US 60/218,006 |
| PRIOR APPLICATION NUMBER: US 60/218,006 |
| PRIOR FILING DATE: 2000-07-29 |
| PRIOR PELING DATE: 2000-04-20 |
| PRIOR FILING DATE: 2000-04-20 |
| PRIOR FILING DATE: 2000-03-29 |
| PRIOR FILING DATE: 2000-03-29 |
| PRIOR FILING DATE: 1999-11-23 |
| PRIOR FILING DATE: 1999-11-23 |
| PRIOR FILING DATE: 1999-01-24 |
| PRIOR FILING DATE: 1999-00-03 |
| PRIOR PRIOR APPLICATION NUMBER: US 60/156,358 |
| PRIOR PRIOR APPLICATION NUMBER: US 60/146,002 |
| PRIOR PRIOR PRIOR PRIOR DATE: 1999-00-09 |
| PRIOR FILING DATE: 1999-00-09 |
| PRIOR FILING DATE: 1999-00-09 |
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| PRIOR APPLICATION NUMBER: US 60/146,002 |
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| PRIOR APPLICATION NUMBER: US 60/146,002 |
| PRIOR APPLICATION NUMBER: US 60/146,002 |
| PRIOR APPLICATION NUMBER: US 60/146,002 |
| PRIOR APPLICATION NUMBER: US 60/146,00
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Pred. No. 1.3e-09;
2; Mismatches 48; Indels 5
    Length 600;
Score 105.4; DB 6; Length
Pred. No. 1.3e-09;
2; Mismatches 48; Indels
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Publication No. US20020198371A1
GENERAL INFORMATION:
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15.1%;
72.9%;
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Best Local Similarity 72.9
Matches 148; Conservative
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US-10-027-632-235943/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
US-10-027-632-235942
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                     282 ATATGTATACATGTGYCATGCTGATGTGCTGCACCCATTAACTCATTTASCATTAGGTAT 223
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                                                                                                                                                                                                                             Sequence 235941, Application US/10027632
; Publication No. US200020407599
; Publication No. US200020407599
; GENERAL INFORMATION:
APPLICANT: Wang, David G
; TITLE OF INVENTION: David G
; TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFRENCE: 108027.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT APPLICATION NUMBER: US 60/219,006
; PRIOR FILING DATE: 2000-09-10
; PRIOR FILING DATE: 2000-09-10
; PRIOR FILING DATE: 2000-09-20
; PRIOR FILING DATE: 2000-09-20
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-11-23
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; PRIOR FILING DATE: 1999-11-23
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-10-3
; RIOR FILING DATE: 1999-10-3
; SEQ ID NOS: 325720
; SEQ ID NO 235941
; TENGTH H. 600
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Publication No. US20030204075A9
GENERAL INFORMATION
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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                                                                                                                222 ATCTCCTAATGCTATCCCTACYC 200
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Best Local Similarity 72.99
Matches 148; Conservative
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US-10-027-632-235941
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282 ATATGTATACATGTGYCATGCTGATGTGCTGCACCCATTAACTCATTTASCATTAGGTAT 223
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Fred. No. 1.3e-
2; Mismatches
CURRENT APPLICATION NUMBER: US/10/027, 632
CURRENT FILING DATE: 2002-04-30
PRIOR FILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR PLICATION NUMBER: US 60/193, 483
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193, 483
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR FILING DATE: 1900-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-8
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
SOFTWARE: 600
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TYPE: DNA
ORGANISM: Homo sapien
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US-10-301-480-578850
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; ORGANISM: Human
US-11-136-623-3
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                                                                                                                                            LENGTH: 82938
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NAME/KEY: 1
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Sequence 3, Application US/09918657

Sequence 3, Application US/09918657

PUBLication No. US20030077773A1

GENERAL INFORMATION:

TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CLO01006-CIP

CURRENT APPLICATION NUMBER: US/09/818,657

CURRENT FILING DATE: 2001-03-28

PRIOR FILING DATE: 2000-12-06

NUMBER OF SEQ ID NOS: 4

SOFTWARE: FASTSED FOR Windows Version 4.0

SEQ ID NO 3
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US-11-136-623-3/c
Sequence 3, Application US/11136623
Sequence 3, Application No. US20050221437A1
GENERAL INFORMATION:
APPLICANT: BRANDON, Rhonda, et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
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Pred. No. 6.6e-09;
0; Mismatches 26; Indels 0;
                                                                           15.1%; Score 105.4; DB 7; Length 600; 72.9%; Pred. No. 1.3e-09; ive 2; Mismatches 48; Indels 5
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82.3%;
                                                                       Query Match
Best Local Similarity 72.99
Matches 148; Conservative
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Best Local Similarity 82.3<sup>3</sup>
Matches 121; Conservative
             ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-235943
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CRGANISM: Human
US-09-818-657-3
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LENGTH: 600
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Sequence 578850, Application US/10301480

Fublication No. US20060057564A1

GENERAL INFORMATION:
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108877.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT PILING DATE: 2002-11-21

FRIOR APPLICATION NUMBER: US 60/311,695

FRIOR APPLICATION NUMBER: US 60/311,695

FRIOR APPLICATION NUMBER: US 60/311,695

FRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FRANCE (Or Windows Version 4.0)

LENGTH: 989
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167,
179,
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214,
226,
                                                                                                                                                                                                                                                          Score 105.4; DB 13; Length 82938; Pred. No. 6.6e-09; 0; Mismatches 26; Indels 0;
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166,
178,
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164,
176,
188,
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211,
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163,
175,
187,
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210,
222,
234,
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TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOOLOG-CIPCOM
CURRENT APPLICATION NUMBER: US/11/136,623
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: 09/730,002
PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
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173,
185,
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208,
220,
232,
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NAME/KEY: misc_feature
LOCATION: 238, 239, 240, 241, 242,
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 82.3%;
Matches 121; Conservative
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LOCATION: 203, 204, 205,
LOCATION: 215, 216, 217,
LOCATION: 227, 228, 229,
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NAME/KEY: misc_feature
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Sequence 214, Application US/10322281 Publication No. US20040126762A1 GENERAL INFORMATION:
                                                             Sequence 51, Application US/11121086 Publication No. US20050266459A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 51
LENGTH: 176760
TYPE: DNA
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Best Local Similarity 80.8%;
Matches 122; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 87.5%;
Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-11-121-086-51
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US-10-322-281-214
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                    RESULT 34
US-11-121-086-51
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Sequence 1192259, Application US/10301480

Publication No. US2006005564A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: 1n the Human Genome

TITLE OF INVENTION: 1n the Human Genome

FILE REFERENCE: 108027.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT FILING DATE: 2002-11-21

PRIOR APPLICATION NUMBER: US 10/215,598

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR APPLICATION NUMBER: US 60/311,695

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FREUESEQ for Windows Version 4.0

SEQ ID NO 1192259

LENGEL DATE: 2001-08-10

LENGEL DATE: 2001-08-10

SEQ ID NO 1192259
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                                                                                                                                                     501 ATTACAGTACTITITAAGTTTTTAGGTACATGTGCACATGTGCAGGTTAGTTACATATGT 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAWE/KEY: misc_feature
LOCATION: 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155,
LOCATION: 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167,
LOCATION: 156, 169, 170, 171, 172, 173, 174, 175, 176, 177, 179, 179,
LOCATION: 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190
OTHER INFORMATION: n = A,T,C or G
FRATURE:
LOCATION: 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202,
LOCATION: 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214,
LOCATION: 227, 228, 229, 330, 231, 232, 233, 234, 235, 236, 237
OTHER INFORMATION: n = A,T,C or G
OTHER INFORMATION: n = A,T,C or G
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                      Gaps
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Best Local Similarity 79.1%; Pred. No. 1.7e-09;
Matches 125; Conservative 0; Mismatches 33; Indels 0;
                      Indels
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                                                                                                                                                                                                                                                                                 561 ATACATGTGCCATGCTGGCGCTGCACCCACTAACTC 598
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                                                                                                                                                                                                                                        124 ATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                      33;
Pred. No. 1.7e-09;
0; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) NAME/KEY: misc_feature

) LOCATION: 238, 239, 240, 241, 242, 243

) CHER INFORMATION: n = A,T,C or G

US-10-301-400-1192259
79.1%;
                      Conservative
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ORGANISM: Homo sapien
Best Local Similarity
Matches 125; Conserv
                                                                                                                                                                                                                                                                                                                                                       RESULT 33
JS-10-301-480-1192259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      561
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20823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: POULSEN, TIM S.
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES FILE REPERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121,086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 0505-05-04
PRIOR FILING DATE: 2004-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                       DB 15; Length 176760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 104.6; DB 8; Length 72678; Pred. No. 8.9e-09; 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REPERENCE: 229452001000
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 TITITITITITGAIGATITITAATAAATATCATTITCTT
                                                                                                                                                                                                                                                                                                                                                                                       Score 104.8; DB 1
Pred. No. 1.1e-08;
0; Mismatches 17
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Sequence 56441, Application US/10301480

| Publication No. US20060057564A1
| Publication No. US20060057564A1
| Publication No. US20060057564A1
| APPLICANT: Wang, David G.
| TITLE OF INVENTION: In the Human Genome
| TITLE OF INVENTION: in the Human Genome
| FILE REFERENCE: 108027.137
| CURRENT APPLICATION NUMBER: US/10/301,480
| CURRENT PILING DATE: 2002-01-21
| PRIOR FILING DATE: 2002-08-09
| PRIOR FILING DATE: 2001-08-10
| PRIOR FILING DATE: 2001-08-10
| NUMBER OF SEQ ID NOS: 1226818
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 564441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 TAAGTITTAGGGTACATGTGCACAATGTGCAGGTTAGTTACATATGTATACATGTGCCAT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.9%; Score 104.2; DB 12;
86.9%; Pred. No. 2.2e-09;
iive 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.9%; Score 104.2; DB 1
86.9%; Pred. No. 2.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 GCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GCTGGTGTGCTGCACCCATTAACTC 157
                   586372 TGCTGCACCCATTAACTCA 586390
144 TGCTGCACCCATTAACTCA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 126; Conservative
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Matches 126; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapien
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                                                                                           RESULT 38
US-10-301-480-564441/c
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                                                                                                                                                COMPOSITIONS AND
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LOCATION: (1)...(1790242)

OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-10-719-993-6940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-719-993-6940

Sequence 6940, Application US/10719993

Publication No. US20040265849A1

Publication No. US20040265849A1

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: ALZHRIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPRENCE: CLO01496

CURRENT APPLICATION NUMBER: US/10/719,993

CURRENT PILING DATE: 2003-11-24

NUMBER OF SEQ ID NOS: 55342

SEQ ID NOS: 55342

SEQ ID NO 6940

LENGTH: 1790242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   586312 TAGGGTACATGTGCACACTGTGCAGGTTACTTACATATGTATACATGTGCCATGCTGGTG 586371
                                                                                                   APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Aziz, Natasha
APPLICANT: Zizonik, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITITIE OF INVENTION: NOVEL METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: Patentin version 3.2
SEQ ID NO 3.1
LENGTH: 126882
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                                                                                                                                                                                                                                                                                                                                                                                            14.9%; Score 104.6; DB 10; Length 126882; 80.8%; Pred. No. 1.1e-08; Live 0; Mismatches 29; Indels 0; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.9%; Score 104.6; DB 9; Length 1790242; 89.2%; Pred. No. 2.5e-08; tive 0; Mismatches 14; Indels 1; Ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89854 TGCCATGCTGGTGCGCTGCACCCGCTAACTC 89884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 TGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                             ; Sequence 321, Application US/10756149; Publication No. US20050181375A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 89.2°
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo Sapiens
US-10-756-149-321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
       RESULT 36
US-10-756-149-321
                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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US-11-121-086-98
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                               241 TAAGTITITAGGGTACATGTGCACAATGTGCAGGTTAGTTACATATGTATACATGTGCCAT 182
92
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                         US-09-944-429-469/C

US-09-944-429-469/C

US-09-944-429-469/C

Sequence 469, Application US/09984429

Publication No. US20040010132A1

GENERAL INFORMATION:

FILE REFERENCE: PZO1820

CURRENT ROSEN et al.

TITLE OF INVENTION: 53 Human Secreted Proteins
FILE REFERENCE: PZ018P2

CURRENT PRIDK DATE: 2001-10-1

PRIOR PILING DATE: 2001-10-1

PRIOR PILING DATE: 1999-04-08

PRIOR PILING DATE: 1999-00-08

PRIOR FILING DATE: 1999-10-09

PRIOR FILING DATE: 1999-10-09

PRIOR FILING DATE: 1997-10-09

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          137 GCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                       137 GCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                             181 GCTGGTGTGCTGCACCATTAACTC 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18833
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RESULT 41 US-10-087-192-238/c ; Sequence 238, Application US/10087192

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Publication No. US2005026645941

GENERAL INFORMATION:

APPLICANT: POULSEN, TIM S.

TITLE OF INVENTION NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

TITLE OF INVENTION NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

TITLE REFERENCE: 09138,6000-00000

CURRENT FILING DAFE: 2005-05-04

CURRENT FILING DAFE: 2004-05-04

NUMBER OF SEQ ID NOS: 107

SOFTWARE: PATENTING DATE: 2004-05-04

NUMBER OF SEQ ID NOS: 107

SEQ ID NO 98

LENGTH: 171732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 TITCTITITITATIATIATACTITITAAGTITITAGGGTACATGTGCAAAGTGTGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 TCACATAAAGTITITITITITITIGATGATTITAATAAAATATCATTITTTTTTTTATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114313 TTAGTTACATATGTATACATGTGCCATGCTGTGTGTGCTGCACCCATTAACTC 114262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 TIAGTIACATATATATACATGTGCCATGCTGGTGCTGCACCCCATTAACTC 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 127369;
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Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morris David W.
APPLICANT: Morris David W.
TITLE OF INVENTION: CANCER
FILE REFERENCE: 52945200122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT APPLICATION NUMBER: US/10/087,192
PRIOR APPLICATION NUMBER: US/10/087,192
PRIOR APPLICATION NUMBER: US/09/747,377
PRIOR PILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US/09/747,377
PRIOR FILING DATE: 2010-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: PRESENCE OF WINDOWS VERSION 4.0
SEQ ID NO 238
LENGTH 127369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 ACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 104; DB 15;
Pred. No. 1.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
14.9%; Score 104; DB 6;
Best Local Similarity 95.5%; Pred. No. 1.4e-08;
Matches 107; Conservative 0; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature; LCCATION: (1)...(127369); OTHER INFORMATION: n = A,T,C or G US-10-087-192-238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3%;
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens
US-11-121-086-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: Unsure
LOCATION: (14335)..(14434)
OTHER INFORMATION: n = any nucleic acid
                                                                                                                                                                        NAME/KEY: Unsure
LOCATION: (16247)..(16346)
OTHER INFORMATION: n = any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Unsure
LOCATION: (59744)..(59744)
OTHER INFORMATION: n = any nucleic acid
FERTURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Unsure
LOCATION: (59749)..(59755)
OOTHER INFORMATION: n = any nucleic acid
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Unsure
LOCATION: (36774)..(36873)
OTHER INFORMATION: n = any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Unsure
LOCATION: (59740)..(59740)
OTHER INFORMATION: n = any nucleic acid
FEAPURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Unsure
LOCATION: (59742)..(59742)
OTHER INFORMATION: n = any nucleic acid
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LOCATION: (36432)..(36433)
DTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc_feature
LCCATION: (36774). (136873)
OTHER INFORMATION: n is a, c, g, or
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LOCATION: (59740)..(59740)
OTHER INFORMATION: n is a, c, g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (59742)..(59744)
OTHER INFORMATION: n is a, c, g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (36293)..(36298)
OTHER INFORMATION: n is a, c, g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (36314)..(36314)
OTHER INFORMATION: n is a, c, g,
                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (16247). (16346)
OTHER INFORMATION: n is a, c
FEATURE:
NAME/KEY: misc_feature
LOCATION: (17457). (17457)
OTHER INFORMATION: n is a, c
                                                                                      NAME/KEY: misc feature
LOCATION: (14335)..(14434)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (21818)..(21818)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (36316) ..(36316)
OTHER INFORMATION: n is a,
                                                                           WESUL 43
Sequence 19, Application US/10517905
Sequence 19, Application US/10517905
Sequence 19, Application US/10517905
Sequence 19, Application World Sequence 19, Sequence 19, Sequence 19, Sequence 19, Sequence 19, Sequence 19, Publication No. US20060084142A1
SEQUENCE INCOMPATION:
APPLICANT: Michael, Health & Science University
APPLICANT: Corless, Christopher Lee
APPLICANT: Demetri, George D.
TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR RECEPTOR TITLE OF INVENTION: ACHHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
TITLE OF INVENTION: ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS
TITLE OF INVENTION NUMBER: US 60/389,107
PRIOR RPLICATION NUMBER: US 60/389,107
PRIOR PILING DATE: 2003-01-08
SOFTWARE: PATCHIN WORSE: US 60/438,899
PRIOR FILING DATE: 2003-01-08
SOFTWARE: PATCHIN VERSION 3.2
SEQ ID NO 19
LANCHH: 191150
39078 ACATGTGCCATGCTGTGCTGCACCCATTAACTC 39113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: n = any nucleic acid FEATURE:
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LOCATION: (10577)..(10676)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
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LOCATION: (10577)..(10676)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Intron
LOCATION: (8978)..(166510)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WAME/KEY: Intron
COCATION: (6286)..(8524)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Intron
(8697)..(8787)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
(8788)..(8977)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
LOCATION: (2331)..(2648)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Intron
(2649)..(4902)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Intron
(5164)..(6154)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WAME/KEY: exon
COCATION: (8525)..(8696)
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(4903)..(5163)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
(6155)..(6285)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Intron
LOCATION: (50)..(2330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: exon
LOCATION: (1)..(49)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: I
LOCATION: (
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LOCATION:
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LOCATION:
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LOCATION:
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FEATURE:
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MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 6; Length 102980;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 14.8%; Score 103.8; DB 6; Length Best Local Similarity 81.6%; Pred. No. 1.4e-08; Matches 120; Conservative 0; Mismatches 27; Indels
                                                                                                                     Sequencial (1330, Application US/10087192)

Publication No. U520020182586A1

GENERAL INFORMATION:

APPLICANT: Morris, David, W.;

APPLICANT: MORIS BANG, Eric K.;

TITLE OF INVENTION: CANCER

TITLE OF INVENTION: CANCER

TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: US/10/087,192

CURRENT APPLICATION NUMBER: US/10/087,192

CURRENT FILING DATE: 2002-03-01

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2001-03-02

NUMBER: OF SEQ 1D NOS: 2059

SOFTWARE: FastSEQ for Windows Version 4.0

SERVING I 1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 17645, Application US/10741600
Publication No. US20050026169A1
GENERAL INFORMATION: Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DET
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FastSEQ for Windows Version 4.0
35311 ACATGTGCCATGCTGTGTGCTGCTGCACCCATTAACTC 35276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84214 ATGCTGGTGCACTGCACCCACTAACTC 84188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Homo sapiens
US-10-087-192-1330
                                                                                       RESULT 44
US-10-087-192-1330/c
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US-10-741-600-17645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 17645
LENGTH: 103660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 102980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 ACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                NAME/KEY: Unsure
LOCATION: (59759)..(59760)
OTHER INFORMATION: n = any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Unsure
LOCATION: (82745)..(82844)
OTHER INFORMATION: n = any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Unsure
LOCATION: (96508)..(96607)
OTHER INFORMATION: n = any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: Unsure
LOCATION: (157152)..(157251)
OTHER INFORMATION: n = any nucleic acid
                                                                                                                                                                                                                                                                                                                                                            LOCATION: (59776)..(59875)
OTHER INFORMATION: n = any nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THER INFORMATION: n = any nucleic acid
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LOCATION: (161475)..(161574)
OTHER INFORMATION: n is a, c, g, or t
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LOCATION: (59776)..(59875)
THER INFORMATION: n is a, c, g,
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NAME/KRY: misc_feature
LOCATION: (157152)..(157251)
OTHER INFORMATION: n is a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AME/KEY: misc feature
LOCATION: (147675)..(147774)
THER INFORMATION: n is a, c,
    LOCATION: (59749)..(59755)
OTHER INFORMATION: n is a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (82745)..(82844)
DIHER INFORMATION: n is a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCATION: (96508)..(96607)
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LOCATION: (147675)..(147774)
                                                                                                                                                      NAME/KEY: misc feature
LOCATION: (59759)..(59760)
OTHER INFORMATION: n is a,
                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (59765)..(59766)
OTHER INFORMATION: n is a,
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OCATION: (96508)..(96
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694

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Sequence 1190576, Application US/10301480

EDBLication No. US20060057564A1

EDBLication No. US20060057564A1

EDBLICANT: Wang, David G.

TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms:
TITLE OF INVENTION: in the Human Genome
FILE REFERENCE: 108027.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT PILING DATE: 2002-08-09

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09949654

Patent No. US20020127644A1

GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO00817

CURRENT APPLICATION NUMBER: US/09/949,654

CURRENT APPLICATION NUMBER: 06/231,572
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                                                                                                                   Gaps
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                                                                           Length 987;
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                                                                                                                                                         4 TITCACATAAAGTITITITITITITGAIGAITITIAAIAAAAIAICAITIT
                                                                       Score 103.6; DB 12; Length
Pred. No. 3.3e-09;
0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                        755 ATACATGTGCCATGCTGTGCTGCTGCACCCATTAACTC 792
                                                                                                                                                                                                                                                                                                                                124 ATACATGTGCCATGCTGGTGCTGCACCCATTAACTC 161
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0; Mismatches
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                                                                    Query Match
Best Local Similarity 78.5%;
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 78.5
Matches 124; Conservative
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; ORGANISM: Homo sapien
US-10-301-480-1190576
           ; ORGANISM: Homo sapien
US-10-301-480-577167
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Sequence 577167, Application US/10301480

Publication No. US20060057564A1

GENERAL INFORMATION:

TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms

TITLE OF INVENTION: in the Human Genome

FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT APPLICATION NUMBER: US 10/215,598

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 2001-08-10

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SEQ ID NOS: 1226818

LENGTH: 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)...(103660)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13253
52865 AGTITIAGGGTACATGTGCACATGTGCAGGTTAGTTACATATGTATACATGTGCCATGC 52924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1323, Application US/10995561
PUDIcation NO. US20050272054A1
GENERAL INFORMATION:
APPLICATION NO. US20050272054A1
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLO01559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004111_24
NUMBER OF SEQ ID NOS: 85702
SOCTWARE: RESEREC for Windows Version 4.0
SSC ID NO 1223
LENGTH: 103660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
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                                                                                                                                                                           52925 TGGTGTACCGCACCCATTAACTC 52947
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                                                                                                                                                    139 TGGTGTGCTGCACCCATTAACTC 161
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ORGANISM: Homo sapiens
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NAME/KEY: misc feature
LOCATION: (1)...(10366)
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Best Local Similarity
Matches 125; Conserv
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RESULT 52
US-10-074-095-661/c
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                                                                                                                                                                                                                                                                                                                           196 TAGTCATTTTCCTAATTGAAAGTATCATAAGTAATCCATAAATTTGAAAAAAATGTTAAC 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 AATTGTAGTTTCAACATTACTTGCAGTTTCAGTTAGTAAATAATAATTAAGCCTAGTAAG 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376 TATAATTTTAATATTGTCAAATAATTTGGAAAATACCATGGGTACTTAATTGATTTTACCA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              496 CAGGAATATCATTGTTAGTTGAATTTTTAGCCTTAGAAAACAAATGGAGTTTAGATAGCT 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    436 AATTTCCATGGAACAAACAAGGTTGGCTATTTTTTGGATTGATATTTTGAAATACTAGTA
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                                                                                                                                                                                                                                                               16 TITITITITITIGALGALTITIAALAAAATAICATITITCITITITATTATACTT
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                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                    Length 368004;
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
                                                                                                                                                                                                  Ouery Match
14.8%; Score 103.6; DB 3;
Best Local Similarity 21.6%; Pred. No. 2.3e-08;
Matches 130; Conservative 0; Mismatches 473;
PRIOR FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12101, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(368004)
OTHER INFORMATION: n = A,T,C or G
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                                                                           TYPE: DNA
ORGANISM: Human
                                                             LENGTH: 368004
                                                                                                                                                                    US-09-949-654-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          616
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LOCATION: (2305)..(2955)
OTHER INFORMATION: 86% homologous to Homo sapiens putative p150,accession number OTHER INFORMATION: U93574,Smith-Waterman Score=1034.
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Pred. No. 1.1e-08;
0; Mismatches 23; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 3200;
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Patent No. US20020094953A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC008
CURRENT APPLICATION NUMBER: US/09/764,860

CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1198
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Score 103.4; DB 1
Pred. No. 5.3e-09;
0; Mismatches 16
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 12101
LENGTH: 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19084 GTGCGCTGCACCTAACT 19065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.6%;
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  / Match 14.8%;
Local Similarity 87.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 113; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 ATTAACTCA 162
                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 51
US-09-764-860-661/c
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LENGTH: 24132
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R APPLICATION NUMBER: 60/251,868
R FILING DATE: 2000-12-08
R APPLICATION NUMBER: 60/229,344
R FILING DATE: 2000-90-01
R FILING DATE: 2000-09-01
R PILING DATE: 2000-09-05
R FILING DATE: 2000-09-02
R PELING DATE: 2000-09-01
R APPLICATION NUMBER: 60/229,343
R FILING DATE: 2000-09-01
R APPLICATION NUMBER: 60/229,287
R FILING DATE: 2000-09-01
R APPLICATION NUMBER: 60/229,287
R FILING DATE: 2000-09-01
R APPLICATION NUMBER: 60/229,513
R APPLICATION NUMBER: 60/239,413
R APPLICATION NUMBER: 60/239,413
R APPLICATION NUMBER: 60/231,413
R APPLICATION NUMBER: 60/231,413
R R FILING DATE: 2000-09-05
                                                                                                                                                                                                                                                                                                                                                                                         R FILING DATE: 2000-09-08
R APPLICATION NUMBER: 60/229,509
R APPLICATION NUMBER: 60/236,367
R FILING DATE: 2000-09-05
R FILING DATE: 2000-09-29
R FILING DATE: 2000-09-29
R FILING DATE: 2000-00-08
R PILING DATE: 2000-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R APPLICATION NUMBER: 60/237,037

R FILING DATE: 2000-10-02

R FILING DATE: 2000-10-02

R FILING DATE: 2000-10-02

R RELING DATE: 2000-10-02

R RELING DATE: 2000-10-20

R RELING DATE: 2000-10-13

R PELLING DATE: 2000-10-13

R PELLING DATE: 2000-10-13

R RELING DATE: 2000-10-13

R RELING DATE: 2000-10-13

R RELING DATE: 2000-10-13

R RELING DATE: 2000-10-13

R RELING DATE: 2000-10-13

R RELING DATE: 2000-10-13

R RELING DATE: 2000-10-13

R RELING DATE: 2000-10-10

R RELING DATE: 2000-10-10

R RELING DATE: 2000-10-10

R RELING DATE: 2000-11-09
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R FILING DATE: 2000-11-08
R APPLICATION NUMBER: 60/249,216
R FILING DATE: 2000-11-17
R APPLICATION NUMBER: 60/249,210
R FILING DATE: 2000-11-17
R APPLICATION NUMBER: 60/226,681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R FILING DATE: 2000-08-14
R APPLICATION NUMBER: 60/227,182
R FILING DATE: 2000-08-22
R APPLICATION NUMBER: 60/225,214
R FILING DATE: 2000-08-14
R APPLICATION NUMBER: 60/235,836
R FILING DATE: 2000-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-10-02
APPLICATION NUMBER: 60/236,370
FILING DATE: 2000-09-29
APPLICATION NUMBER: 60/236,802
FILING DATE: 2000-10-02
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APPLICATION NUMBER: 60/249,213
FILING DATE: 2000-11-17
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APPLICATION NUMBER: 60/225,759
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FILING DATE: 2000-09-06
APPLICATION NUMBER: 60/215,135
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APPLICATION NUMBER: 60/249,218
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APPLICATION NUMBER: 60/225,213
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                                                            THILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies THILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies THILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies CORRENT APPLICATION NUMBER: UG/10/074,095

CORRENT APPLICATION NUMBER: UG/10/074,095

PRIOR FILING DATE: 2002-02-14

PRIOR FILING DATE: 2006-01-31

PRIOR FILING DATE: 2006-01-31

PRIOR PLING DATE: 2006-01-31

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PRIOR P
Sequence 661, Application US/10074095
Publication No. US20030077704A1
GENERAL INFORMATION:
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FILING DATE: 2000-10-20
APPLICATION NUMBER: 60/244,617
FILING DATE: 2000-11-01
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FILING DATE: 2000-09-29
APPLICATION NUMBER: 60/251,856
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Gaps
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APPLICANT: David W. Morris
APPLICANT: David W. Morris
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REPRENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330, 773
CURRENT PILING DATE: 2002-12-27
NUMBER OF SEQ IO NOS: 981
SOFTWARE: FASEURO FOR Windows Version 4.0
                                                                                                  APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC008C2
CURRENT APPLICATION NUMBER: US/10/212,872
CURRENT FILING DATE: 2002-08-07
Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 1198
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 661
LENGTH: 24132
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Pred. No. 1.1e-08;
0; Mismatches 23;
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                   Sequence 661, Application US/10212872
Publication No. US20030215893A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 76, Application US/10330773 Publication No. US20060040262A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 GTGTGCTGCACCCATTAACT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.6%;
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 83.6
Matches 117; Conservative
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                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-10-212-872-661
US-10-212-872-661/c
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LENGTH: 118544
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US-10-330-773-76/c
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14.7%; Score 103.2; DB 6;
Best Local Similarity 83.6%; Pred. No. 1.1e-08;
Matches 117; Conservative 0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/232,081
PRIOR FILING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
PRIOR PELING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/231,414
PRIOR APPLICATION NUMBER: 60/231,244
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/233,063
PRIOR PILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/233,39
PRIOR PELING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,39
PRIOR PELING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/232,39
PRIOR PELING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/231,39
PRIOR APPLICATION NUMBER: 60/231,399
PRIOR PELING DATE: 2000-10-20
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PRIOR PELING DATE: 2000-11-20
                      PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,207
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,245
PRIOR FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,244
PRIOR APPLICATION NUMBER: 60/249,247
PRIOR APPLICATION NUMBER: 60/249,217
PRIOR FILING DATE: 2000-11-17
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R FILING DATE: 2000-11-17

NR APPLICATION NUMBER: 60/249,215

NR APPLICATION NUMBER: 60/249,264

NR APPLICATION NUMBER: 60/249,264

NR APPLICATION NUMBER: 60/249,214

NR APPLICATION NUMBER: 60/249,214

NR APPLICATION NUMBER: 60/249,214

NR APPLICATION NUMBER: 60/249,214

NR FILING DATE: 2000-11-17

NR APPLICATION NUMBER: 60/249,297

NR APPLICATION NUMBER: 60/249,297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/231,242
FILING DATE: 2000-09-08
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RESULT 53

RESULT 55 US-10-301-480-570607

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Sequence 1166170, Application US/10301480

Bublication No. US20060057564A1

GENERAL INFORMATION:
TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: In the Human Genome
FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT APPLICATION NUMBER: US 10/215,598

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 997
                                                                                                                                                                                                                                                                         APPLICANT: Wang, David G.

TITLE OF INVENTION: In the Human Genome
TITLE OF INVENTION: In the Human Genome
TITLE OF INVENTION: In the Human Genome
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TITLE OF INVENTION: In the Human Genome
TITLE OF INVENTION: In the Human Genome
TITLE OF INVENTION: In the Human Genome
CURRENT PILLING DATE: 2002-11-21
PRIOR FILLING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR FILLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR APPLICATION NUMBER: US 60/311,695
PRIOR APPLICATION NUMBER: US 60/311,695
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                                             772 ATGCTGGTGTGTGCTGCACCCACTAACTC 798
                                                                                                                                                RESULT 57
US-10-301-480-552761/c
Sequence 552761, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
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Best Local Similarity 82.5%;
Matches 118; Conservative
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ORGANISM: Homo sapien
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; ORGANISM: Homo sapien
US-10-301-480-1166170
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US-10-301-480-1166170/c
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Sequence 570607, Application US/10301480

Publication No. US200600575641

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms:

TITLE OF INVENTION: In the Human Genome

FILE REFERENCE: 108827.137

CURRENT APPLICATION NUMBER: US/10/301,480

CURRENT PILING DATE: 2002-11-21

PRIOR FILING DATE: 2002-11-21

PRIOR FILING DATE: 2002-08-09

PRIOR FILING DATE: 2001-08-10

NUMBER OF SEQ ID NOS: 1226818

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 865
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: In the Human Genome
FILE REPERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT APPLICATION NUMBER: US/10/312,598
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2002-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: PASISEQ for Windows Version 4.0
LENGTH: 865
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14.7%; Score 103; DB 12;
Best Local Similarity 85.7%; Pred. No. 4.1e-09;
Matches 126; Conservative 0; Mismatches 20;
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Matches 126; Conservative
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US-10-301-480-570607
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US-10-301-480-1184016
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
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Best Local Similarity 81.5%;
Matches 119; Conservative (
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; ORGANISM: Human
US-10-027-632-256998
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             TITATITIATITITIGEGEGIAITIATITATITATITATITATITATITACITATITAA 434
                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108027.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/199,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 1000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-10-3
PRIOR FILING DATE: 1999-09-10-3
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTESE FOR WINDOWS VERSION 4.0
SEQ ID NO 256997
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Publication No. US20020198371A1
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFREENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
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14.7%; Score 102.8; DB 6; Length 729;
Best Local Similarity 81.5%; Pred. No. 4.2e-09;
Matches 119; Conservative 0; Mismatches 27; Indels 0
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US-10-027-632-256997
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200 TTAAGTTTTTAGGGTACATGTGCACACACGGTTTGTTACATATGTATAAATGTGCCA 141
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
PRIOR PLICATION NUMBER: US 60/218,006
PRIOR PLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR PLICATION NUMBER: US 60/185,218
PRIOR PLICATION NUMBER: US 60/186,388
PRIOR FILING DATE: 1999-11-23
PRIOR PLICATION NUMBER: US 60/146,002
PRIOR PLING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PASSEE OF WINDOWS VETSION 4.0
SEQ ID NO 256997
LENGTH...729
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Score 102.8; DB 6; Length Pred. No. 4.2e-09; O; Mismatches 27; Indels
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
ITTLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
FRIOR PILING DATE: 2000-07-12
PRIOR PLICATION NUMBER: US 60/218,006
PRIOR PLICATION NUMBER: US 60/198,676
PRIOR PLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-04-20
PRIOR PLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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Pred. No. 4.2e-09;
0; Mismatches 27; Indels
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Matches 119; Conservative
                 Matches 119; Conservative
Best Local Similarity
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US-10-027-632-256998/c
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APPLICANT: Wang, David G. TILLE OF INVENTION: Identifiction and Mapping of Single Nucleotide Polymorphisms

US-10-301-480-91798/c ; Sequence 91798, Application US/10301480 ; Publication No. US20060057564A1 ; GENERAL INFORMATION:

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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
TITLE OF INVENTION: in the Human Genome
TITLE OF INVENTION: in the Human Genome
FILE REPERENCE: 108827.137
CURRENT APPLICATION NUMBER: US/10/301,480
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/215,598
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 1226818
SOFTWARE: FASISEQ for Windows Version 4.0
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Pred. No. 4.2e-09;
0; Mismatches 27; Indels
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FILE OF INVENTION: in the Human Genome FILE REFERENCE: 108827.137 CURRENT APPLICATION NUMBER: US/10/301,480 CURRENT FILING DATE: 2002-11-21 PRIOR APPLICATION NUMBER: US 60/311,695 PRIOR FILING DATE: 2002-08-09 PRIOR FILING DATE: 2001-08-10 NUMBER OF SEQ ID NOS: 1226818 SOFTWARE: PASTSEQ for Windows Version 4.0 SEQ ID NO9: 1729
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; Sequence 91799, Application US/10301480
; Publication No. US20060057564A1
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Best Local Similarity 81.5%;
Matches 119; Conservative
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US-10-301-480-91798
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ORGANISM: Homo
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LENGTH: 729
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Patent No. US20020061521A1
GENERAL, INFORMATION:
BAPPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT APPLICATION NUMBER: US/09/764,869
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 102.8; DB 8; DB 9; Pred. No. 3e-08;
                                                                                                                                                          US-10-367-094-83/c
; Sequence 83, Application US/10367094
; Publication No. US20040170982A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer; FILE REFERENCE: 529452001500
; CURRENT APPLICATION NUMBER: US/10/367,094
; CURRENT FILING DATE: 2003-02-14
; NUMBER OF SEQ 1D NOS: 203
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 102.6; DB 3; Length
Pred. No. 1.5e-08;
0; Mismatches 19; Indels
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                                             136 TGCTGGTGTGCTGCACCCATTAACTC 161
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Best Local Similarity 86.2%;
Matches 125; Conservative
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Best Local Similarity
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LENGTH: 26225
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; Sequence 705208, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: In the Human Genome
; TITLE OF INVENTION: In the Human Genome
; TITLE OF INVENTION: In the Human Genome
; TITLE OF INVENTION: In the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR PILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SEQ ID NO 705208

LENGTH: 729
RESULT 65
US-10-301-480-705207/c
; Sequence 705207/c
; Sequence 705207, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: In the Human Genome
FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 705207
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Pred. No. 4.2e-09;
0; Mismatches 27; Indels
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Best Local Similarity 81.5%; Pred. No. 4.2e-09;
Matches 119; Conservative 0; Mismatches 27
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Best Local Similarity 81.5%;
Matches 119; Conservative
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; ORGANISM: Homo sapien
US-10-301-480-705208
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US-10-301-480-705207
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US-10-301-480-705208/c
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86.2%; Pred. No. 1.5e-08;
tive 0; Mismatches 19;
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Matches 125; Conservative
; LENGTH: 26225
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-091-504-1276
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; Bequence 1276, Application US/10091504
; Publication No. US20030059908A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PCOO7C1
; CURRENT APPLICATION NUMBER: US/10/091,504
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2442
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1276
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0; Mismatches 19
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Matches 125; Conservative
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ORGANISM: Homo sapiens
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Sequence 557, App
Sequence 596, App
Sequence 58055, App
Sequence 25751, A
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Sequence 197223,
Sequence 29041, A
Sequence 2011, Appl
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Sequence 2011, Appl
Sequence 20514, Appl
Sequence 61303, A
Sequence 61303, A
Sequence 207140,
Sequence 386, Appl
Sequence 209478,
Sequence 209478,
Sequence 60109, A
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28210, A
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2: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*

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8: /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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                                                              July 19, 2006, 07:08:55 ; Search time 286 Seconds
       GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-517-441-283
US-10-517-441-287
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US-10-505-928-596
US-11-266-748A-58095
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US-11-266-748A-197923
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US-11-266-748A-23292
US-11-266-748A-205304
US-10-539-228-826
US-11-266-748A-61303
US-11-266-748A-61303
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US-11-266-748A-209478
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US-11-260-842-1
US-11-266-748A-28210
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Maximum Match 100%
Listing first 70 summaries
                                           - nucleic search, using sw model
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25150, A
60108, A
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79, Appl
29045, A
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60144, A
50139, A
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Sequence 196825, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Harkin, Paul

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 55815-0102 (1319189)

CURRENT APPLICATION WUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

FRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR PILING DATE: 2004-11-03

FRIOR APPLICATION NUMBER: EP 04105483.4

FRIOR APPLICATION NUMBER: EP 04105483.4

FRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

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PRIOR PILING DATE: 2004-11-03

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PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03
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US-11-266-748A-511402
US-10-519-335-37
US-11-266-748A-59086
US-11-266-748A-22038
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APPLICANT: HOBFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
TITLE OF INVENTION: proliferative disorders
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                                                                    72 ACTITIAAGTITIAGGGTACATGTGCAAAGTGTGCAGGTTAGTTACATATATACATGT
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      Pred. No. 3.2e-10;
0; Mismatches 324; Indels
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CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR PELING DATE: 2003-10-01
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; Publication No. US20060121467A1
; GENERAL INFORMATION:
; APPLICANT: FOEKENS, John
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMRICH, Inko
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SCHMITT, Armin
SCHMITT, Manfred
                          Matches 312; Conservative
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        Best Local Similarity
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APPLICANT: PERENEX, John
APPLICANT: RABBECK, Nadia
APPLICANT: MARBECK, Nadia
APPLICANT: MARRES, Sabine
APPLICANT: MARTENS, John
APPLICANT: MARTENS, John
APPLICANT: MARTENS, John
APPLICANT: MIWRICH; Inko
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APPLICANT: SCHMITT, Ammin
APPLICANT: SCHMITT, Ammin
APPLICANT: SCHMITT, Ammin P.
APPLICANT: SCHMITT, Ammin P.
APPLICANT: COCK, Maxime P.
APPLICANT: LOCK, Maxime P.
APPLICANT: MORENEX, Heinz
APPLICANT: MARK, Ammin P.
APPLICANT: MORENEX: Meinz
TITLE OF INVENTION: Proliferative disorders
FILE REPERENCE: 17675-93
CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10310956.8
PRIOR APPLICATION NUMBER: DE 1031096.8
PRIOR FILING DATE: 2003-10-07
PRIOR FILING DATE: 2003-10-07
PRIOR FILING DATE: 2003-10-07
PRIOR SEQ ID NOS: 2147
SEQ ID NO 203
LENGTH: 8666
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                                                                                                                                                                                                                                                                                                                              Length 1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 8666;
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                         Score 110.8; DB 8;
Pred. No. 4.9e-11;
0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                16 TITITITITITICATGATTTTAATAAAATATCATTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.2%; Score 106.6;
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
SEQ ID NO 196825
LENGTH: 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 283, Application US/10517441 Publication No. US20060121467A1
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 84.9%;
Matches 124; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-196825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-517-441-283
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Indels

Length 72678;

DB 6;

Score 104.6; DB 6; Pred. No. 8.7e-10; 0; Mismatches 29;

14.9%;

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TACTITITAAGITITIAGGGTACATGTGCAAAGTGTGCCAGGTTAGTTACATATATACATG 130
                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/539,228
CURRENT FILING DATE: 2005-06-17
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-18
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 214
LENGTH: 72678
                                                                                                                                                                                                                          Query Match
Best Local Similarity 80.8
Matches 122; Conservative
                                                                                                                                                      TYPE: DNA
CORGANISM: Homo sapiens
US-10-539-228-214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1607 TATTITTAAGITTITAGAGIATATGIGTATAATGIGTAGGITTGTTATATATGTATATGT 1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1667 GITATGITGGIGITGITTTATTATTA-TTA-TTAGTATTAGGATATATTTTTAAT 1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .966 GTTATATATATTTTTTATAAGAGTTGAAAGAGTTTTTGATGTAGGAATTTATGGTAGAGT 2025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 GCCATGCTGGTGTGCTGCACCCATTAACTCACATGAAGTTTTTTTAAATTTTTAGTGACA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252 TAACTACTCTGATAAAAAGTTTTATAGTTTCCTACTTTTAAGCAAAATTCCATAGGGCA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        192 GITITIAGICATITICCIAATIGAAAGIATCATAAGIAATCCATAAATITIGAAAAAAAGI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 TAAGTATAATTTAATATTGTCAAATAATTTGGAAAATACCATGGGTACTTAATTGATTTT 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                432 ACCABATTTCCATGGAACAAACAAGGTTGGCTATTTTTGGATTGATATTTTGAAATACT 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        492 AGTACAGGAATATCATTGTTAGTTGAATTTTTAGCCTTAGAAAACAAATGGAGTTTAGAT 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             552 AGCTAAAGTATAATTTGTGATTTAATAATGGTATGGAGTTAGGGCTATGATAATTA 611
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                                                                                                                                                                                                                          OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                          15.2%; Score 106.6; DB 6; Length 8666; ilarity 49.0%; Pred. No. 3.2e-10; Conservative 0; Mismatches 324; Indels 1;
                                                                                                                                                                                                                                                                                                                                                      GATGATTTTAATAAAATATCATTTTCTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGAAAACACCCAAGAATGTTTTATACTTTTAAATTT 648
PRIOR APPLICATION NUMBER: DE 103100056.8
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR PILING DATE: 2003-01-07
PRIOR PILING DATE: 2002-10-01
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 214, Application US/10539228; Publication No. US20060154250A1; GENERAL INFORMATION:
                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                             Local Similarity
hes 312; Conserv
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                                                                                                                                                                       TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 70665;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 14.8%; Score 103.4; DB 6; Length Best Local Similarity 87.6%; Pred. No. 1.4e-09; Matches 113; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                            al.
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                                                                                                                                                                                                                                                                      APPLICANT: Ludwig Institute for Cancer Research TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES FILE REFERENCE: 28967/139178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR PLILING DATE: 2004-08-27
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: Patentin 3.2
                                                                                                     68661 recenterrecreerecacecernaere 68691
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                                                                                                                                                                                                          ; Sequence 596, Application US/10505928; Publication No. US20060088532A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62874 CATTAACTC 62882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
COGANISM: Homo sapiens
US-10-505-928-596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
US-11-266-748A-58095/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 596
LENGTH: 70665
                                                                                                                                                                                        US-10-505-928-596
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APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: CHIR0052-101 (PP023370.0003)

Gaps

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16 TITITITITITIGAIGATITITAATAAAATATCATTITICITITITITATTATTATACTT
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                                                                                                                                                                                                                                             DB 8; Length 1577;
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| Sequence 197923, Application US/11266748A
| Publication No. US20060134663A1
| GENERAL INFORMATION:
| APPLICANT: Harkin, Paul
| APPLICANT: Harkin, Paul
| APPLICANT: Harkin, Paul
| APPLICANT: Mulligan, Kari
| TITLE OF INVENTION: Methods of Using the Same
| TITLE OF INVENTION: Methods of Using the Same
| TITLE OF INVENTION: Methods of Using the Same
| TITLE OF INVENTION: Methods of Using the Same
| TITLE OF INVENTION: Methods of Using the Same
| TITLE OF INVENTION: Methods of US,11/266,748A
| TITLE OF INVENTION: MUMBER: ED 04105479.2
| PRIOR FILING DATE: 2004-11-03
| PRIOR FILING DATE: 2004-11-03
| PRIOR PILING DATE: 2004-11-03
| PRIOR PILING DATE: 2004-11-03
| PRIOR APPLICATION NUMBER: EP 04105485.9
| PRIOR PILING DATE: 2004-11-03
| PRIOR PILING DATE: 2004-11-03
| PRIOR FILING DATE: 2004-11-03
| PRIOR FILING DATE: 2004-11-03
| PRIOR FILING DATE: 2004-11-03
| PRIOR FILING DATE: 2004-11-03
| PRIOR FILING DATE: 2004-11-03
| PRIOR PILING DATE: 2004-11-03
| PRIOR FILING DATE: 2004-11-03
| PRIOR PILING DATE: 2004-11-03
| PRIOR FILING DATE: 2005-07-18
| PRIOR APPLICATION NUMBER: US 60/662,276
| PRIOR PILING DATE: 2005-07-18
| PRIOR PILING DATE: 2005-07-18
| PRIOR PILING DATE: 2005-07-18
| PRIOR PILING DATE: 2005-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1000;
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                                                                                                                                                                                                                                           Score 100.4; DB 8;
Pred. No. 3.4e-09;
0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
14.3%; Score 99.8; DB 8;
Best Local Similarity 73.1%; Pred. No. 4.1e-09;
Matches 128; Conservative 0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1454 TGCTGGTGTGCTGCACCCACTAACTC 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 TGCTGGTGTGCTGCACCCATTAACTC 161
PRIOR FILING DATE: 2005-03-14
PRIOR PELLING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PALENTIN VERSION 3.3
SEQ ID NO 25751
LENGTH: 1577
                                                                                                                                                                                                                                           14.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.3 SEQ ID NO 197923
                                                                                                                                                                                                                                                                                      Matches 124; Conservative
                                                                                                                                                                            ; ORGANISM: Homo Sapiens
US-11-266-748A-25751
                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-11-266-748A-197923
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ORGANISM:
                                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                    Local
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             Length 1615;
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APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Miligan, Karl
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55615-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2006-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PAPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 04662,276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.5%; Score 101.6; DB 8; 86.1%; Pred. No. 2.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 86.1
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo Sapiens
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SEQUENCE 21229 Application No. US20060134663A1

SEDERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: TRANSCRIPTOME MICROARRAY Technology and

TITLE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 55815-0102 (319189)

CURRENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR PELING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

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PRIOR FILING DATE: 2005-03-14
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Pred. No. 7.8e-09;
0; Mismatches 27; Indels
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         Methods of Using the Same
                          FILE REFERENCE: 55815-0102 (119189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
                                                                                                              PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
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PRIOR PILING DATE: 2005-07-18
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Best Local Similarity 81.9%;
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Sapiens
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APPLICANT: SCHMITT, Manfred
APPLICANT: SCHMITT, Manfred
APPLICANT: SCHMITT, Manfred
APPLICANT: LOOK, Maxime P.
APPLICANT: MAX: Almuth
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
TITLE OF INVENTION: MORER: 2004-12-11
PRIOR APPLICATION NUMBER: US/10/517,441
CURRENT APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-01-07
PRIOR PLILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 1030096.8
PRIOR PLILING DATE: 2003-01-07
PRIOR APPLICATION NUMBER: DE 10245779.4
PRIOR PLILING DATE: 2002-10-07
PRIOR PLILING DATE: 2002-10-01
PRIOR PLILING DATE: 2002-10-07
PRIOR PLILING DATE: 2002-10-07
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122 ATATACATGTGCCATGCTGCTGCACCCATTAACTCACATGAAGTTTTTT 176
                                                                                                                                                            Gaps
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Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 99.8; DB 6; Length 8 Pred. No. 5e-09; 0; Mismatches 32; Indels
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                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/10517441 Publication No. US20060121467A1 GENERAL INFORMATION:
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78.8%;
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MODEL, Fabian
NIMMRICH, Inko
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Best Local Similarity 78.8
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: FOEKENS, John APPLICANT: HARBECK, Nadia APPLICANT: KOENIG, Thomas APPLICANT: MAIER, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RUJAN, Tamas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo Sapiens
US-10-517-441-19
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RESULT 14
US-11-266-748A-61303
is Sequence 61303, Application US/11266748A
is Sequence 61303, Application US/11266748A
is Sequence 61303, Application US/11266748A
is Publication No. US20060134663A1
is APPLICANT: Harrin, Paul
is APPLICANT: Mulligan, Karl
itTLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same itTLE OF INVENTION: Wethods of Using the Same itTLE OF INVENTION: UNMER: US/11/266,748A
icurrant Filling DATE: 2005-11-03
ip RIOR APPLICATION NUMBER: EP 04105482.6
ip RRIOR FILING DATE: 2004-11-03
ip RRIOR FILING DATE: 2004-11-03
ip RRIOR FILING DATE: 2004-11-03
ip RRIOR FILING DATE: 2004-11-03
ip RRIOR FILING DATE: 2004-11-03
ip RRIOR PLING DATE: 2004-11-03
ip RRIOR APPLICATION NUMBER: EP 04105507.0
ip RRIOR APPLICATION NUMBER: EP 04105485.9
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ip RRIOR APPLICATION NUMBER: EP 04105485.9
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Pred. No. 9.1e-09;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1).__(83965); OTHER INFORMATION: n = A,T,C or G US-10-539-228-826
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Best Local Similarity 93.4%;
Matches 114; Conservative
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                                                                                                                                                                                                                                      Score 99.6; DB 8; Length 122568; Pred. No. 6.8e-09; 0; Mismatches 29; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Harrin, Paul
APPLICANT: Harrin, Paul
APPLICANT: Harrin, Paul
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 58815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 0410548.6
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
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PRIOR PELING DATE: 2005-07-18
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Pred. No. 5.2e-09;
0; Mismatches 38; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 ATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
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PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PAECHLIN VERSION 3.3
SEQ ID NO 23292
LENGTH: 122568
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Best Local Similarity 76.2%;
Matches 122; Conservative
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 81.0%;
Matches 128; Conservative
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                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23292
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US-11-266-748A-205304
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20766 AATGTGCAGGTTAGTTACATATGTATACATGTGCCATGCTGGTGTGCTGCACCCATTAAC 20707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 AGTGTGCAGGTTAGTTACATATACATGTGCCATGCTGGTGCTGCACCCATTAAC
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                                                                                            RESULT 13
US-10-539-228-826/C
| Sequence 826, Application US/10539228
| Sequence 826, Application US/10539228
| Publication No. US20060154250A1
| GENERAL INFORMATION:
| APPLICANT: David W. Morris
| APPLICANT: Marc S. Malandro
| TITLE OF INVENTION: Novel Compositions and Methods in Cancer FILE REFERENCE: CHIRODS-101 (PP023370.0003)
| CURRENT APPLICATION NUMBER: US/10/539,228
| CURRENT APPLICATION NUMBER: US/10/539,228
| PRIOR APPLICATION NUMBER: US 10/322,281
| PRIOR PILING DATE: 2005-06-17
| PRIOR PILING DATE: 2005-06-18
| NUMBER OF SEQ ID NOS: 866
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 83965;
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729 Grafacargieccargeregreecerecaccacraacre 768
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14.0%; Score 97.8; DB 6; Length 301477; 80.9%; Pred. No. 1.5e-08;
                                                                                                                                                                                                                                                                                            Sequence 456, Application US/10539228
| Publication No. US2006015425041
| GENERAL INFORMATION:
| APPLICANT: David W. Morris
| APPLICANT: David W. Morris
| APPLICANT: David W. Morris
| APPLICANT: David W. Morris
| TILE OF INVENTION: NOVel Compositions and Methods in Cancer; FILE REFERENCE: CHIRO52-101 (PP023370.003)
| CURRENT APPLICATION NUMBER: US/10/539,228
| CURRENT APPLICATION NUMBER: US 10/322,281
| PRIOR APPLICATION NUMBER: US 10/322,281
| PRIOR PILING DATE: 2005-10-18
| NUMBER OF SEQ ID NOS: 866
| SOFTWARE: FeatSEQ for Windows Version 4.0
| LENGTH: 301477
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Publication No. US20060154250A1

GENERAL INFORMATION:

APPLICANT: David W. Morris

TITLE OF INVENTION: Novel Compositions and Methods in Cancer

FILE REFERENCE: CHIRODS-101 (PP023370.003)

CURRENT FILING DATE: 2005-06-17

PRIOR PPLICATION NUMBER: US/10/539,228

CURRENT FILING DATE: 2002-12-18

NUMBER OF SEQ ID NOS: 866

SOFTWARE FELSE FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                      536 GCTGGTGTGCTGCACCCATTAACTC 560
                                                                                                                                              137 GCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80011 Grerecrececcarracere 79991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:

NAME/KEY: misc feature

LOCATION: (1)...(301477)

OTHER INFORMATION: n = A,T,C or G
US-10-539-228-456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 386
LENGTH: 52987
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                  US-10-539-228-456/c
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                                                                                                                                                                                                                                                                                                                                                                                                                       104894 TTAAGTTTTTAGGGTACTTGTGCACAACGTGCAGGTTTGTTACATATGTATACATGTGCCA 104953
                                                                                                                                                                                                                                                                                                                                                     ٦;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MULIGAN, Patrick
APPLICANT: Muligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
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PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE PLEING UN VERSION 3.3
                                                                                                                                                                                                                                                                                                     14.1%; Score 98.8; DB 8; Length 110
84.2%; Pred. No. 9.4e-09;
ive 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 84.1%; Pred. No. 9.2e-09;
Matches 122; Conservative 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104954 TGTTGGTGTGCTGCACCATTAACTC 104979
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PATCHIN VERSION 3.3
SEQ ID NO 61303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 TGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 207140, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                Query Match . 14.1%
Best Local Similarity 84.2%
Matches 123; Conservative
                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-61303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: Homo Sapiens
US-11-266-748A-207140
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US-11-266-748A-207140
                                                                                                                                                                                      LENGTH: 110096
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LENGTH: 1000
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Gaps

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28779 -TAAGTITIAGGGTACATGTGCACATICTGCAGGTTAGTTACATATGTATACATGTGCA 28721
                                                                      7
                                                                                                                                                                                                                                         16 TITITITITITICATGATITITAATAAATATCATITITCTITITITITATTATTATACTT
                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
Score 97.4; DB 6; Length 52987;
Pred. No. 1.5e-08;
0; Mismatches 21; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Johnston, Patrick
APPLICANT: Muligan, Karl
ITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT PELLING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: UP 04105492.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PELLOR DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PELLING DATE: 2004-11-03
PRIOR PELLING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR PELLING DATE: 2005-01-18
PRIOR PELLING DATE: 2005-01-18
PRIOR PELLING DATE: 2005-01-18
PRIOR FILING DATE: 2005-01-18
PRIOR FILING DATE: 2005-01-18
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13.9%; Score 97.2; DB 8; Length 638;
Best Local Similarity 78.0%; Pred. No. 1.1e-08;
Matches 117; Conservative 0; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCATGTTGGTGTGCTGCACCCGTTAACTC 346
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                                                                                                                                                                                                                                                                                                                                                                                      28720 TGCTGGTGCGCTGCACCCACTAA 28698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 209478, Application US/11266748A
Publication No. US20060134663A1
GRNERAL INFORMATION:
APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                   TGCTGGTGTGCTGCACCCATTAA 158
        Query Match
Best Local Similarity 84.6%;
Matches 121; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo Sapiens
US-11-266-748A-209478
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RESULT 19

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192551 TITIATTATACTITAAGTITTTAGGGTACATGTGCACATTGTGCAGGTTAGTTACATATGT 192610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 301477;
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Sequence 456, Application US/10539228
| Publication No. US20060154250A1
| GENERAL INPORMATION:
| APPLICANT: David W. Morris
| APPLICANT: Marc S. Malandro
| TITLE OF INVENTION: Novel Compositions and Methods in Cancer
| FILE REFERENCE: CHIR0052-101 (PP023370.0003)
| CURRENT APPLICATION NUMBER: US/10/539,228
| CURRENT FILING DATE: 2005-06-17
| PRIOR FILING DATE: 2005-12-18
| NUMBER OF SEQ ID NOS: 866
| SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-11-266-748A-60109
US-11-266-748A-60109
IS Sequence 60109, Application US/11266-748A
Publication No. US20060134663A1
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Kari
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
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2e-08;
thes 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192611 ATACATGTGCCATGCTGGTGCGCTGCACTAACTC 192648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 ATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 97.2; Di
Pred. No. 2e-0
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature; ICCATION: (1)...(301477); CTHER INFORMATION: n = A,T,C or GUS-10-539-228-456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 13.9%;
Best Local Similarity 75.9%;
Matches 120; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-266-748A-60109
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 456
LENGTH: 301477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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APPLICANT: Vance, Jeffrey M.
APPLICANT: Vance, Jeffrey M.
APPLICANT: Kraus, William E.
APPLICANT: Goldschmidt, Pascal J.
APPLICANT: Goldschmidt, Pascal J.
APPLICANT: Gregory, Simon G.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CORRELATING GENETIC MARKERS WITH
TITLE OF INVENTION: CARDIOVASCULAR DISEASE
FILE REPERBUCE: 5405-347
CURRENT APPLICATION NUMBER: US/11/260,842
CURRENT APPLICATION NUMBER: US 60/662,447
PRIOR FILING DATE: 2004-10-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 IGTITCACATAAAGTITITITITITITITITATAAAATATCATTITITITA
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                                                                                                              WESULT 226

WESULT 226

WESULT 226

WESULT 226

WEDLICART 31545, Application US/11266748A

PUBLICARTAL UNSORANTION.

APPLICANT: Harkin, Paul

APPLICANT: Harkin, Paul

APPLICANT: Harkin, Paul

TITLE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 55815-0102 (139189)

CURRENT APPLICATION WHERE: US/11/266,748A

FILE REFERENCE: 55815-0102 (139189)

CURRENT PILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR PELING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

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PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR APPLICATION NUMBER: EP 04105484.2

PRIOR APPLICATION NUMBER: US 60/662,276

PRIOR PILING DATE: 2005-01-18

PRIOR PILING DATE: 2005-03-14

PRIOR PILING DATE: 2005-03-14

PRIOR PILING DATE: 2005-03-14

PRIOR PILING DATE: 2005-03-14

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Pred. No. 1.4e-08;
0; Mismatches 32; Indels 1
      562 GTATACATGTGCCATATTGGTGTGCTGCACCCATTAACTC 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                439 GTATACATGTGCCATATTGGTGTGCTGCACCCATTAACTC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 ATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
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Publication No. US20060115845A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 79.4%;
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo Sapiens
US-11-266-748A-341545
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APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: MUMBER: ED 04105479.2
PRIOR PAPLICATION NUMBER: EP 04105479.2
PRIOR PELLING DATE: 2004-11-03
PRIOR PAPLICATION NUMBER: EP 04105483.4
PRIOR PELLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PELLING DATE: 2004-11-03
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PRIOR PELLING DATE: 2005-01-14
PRIOR PELLING DATE: 2005-07-18
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PRIOR PELLING DATE: 2005-07-18
                                                                                                                                                           Score 97; DB 8; Length 131546; Pred. No. 2e-08;
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Pred. No. 1.4e-08;
0; Mismatches 32;
                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                           13.9%;
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Best Local Similarity 79.4%;
Matches 127; Conservative
                                                                                                                                                    Query Match
Best Local Similarity 75.21
Matches 121; Conservative
                               ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-60109
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US-11-266-748A-290116
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LENGTH: 131546
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136 TGCTGGTGTGCTGCACCCATTAAC 159
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Best Local Similarity 84.0%; Pred. No. 2.4e-08;
Matches 121; Conservative 0; Mismatches 22; Indels 1;
                                                                                                                                                                                                Length 261789;
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                Query Match
13.8%; Score 96.8; DB 8;
Best Local Similarity 84.0%; Pred. No. 2.3e-08;
Matches 121; Conservative 0; Mismatches 22;
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CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT PILING DATE: 2005-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
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PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-07-14
PRIOR SPELICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
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Sequence 28210, Application US/11266748A;
Publication No. US20060134663A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGGTGTGCTGCACCCATTAACT 160
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1
LENGTH: 261789
                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
US-11-260-842-1
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US-11-266-748A-28210
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LENGTH: 421987
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926 TTAAGTTTTTAGGGTACATGTGCACAACGTGCAGGTTTGTTACATATGTATACATGTGCCA 867
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TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
CURRENT APPLICATION UNDBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 040662,276
PRIOR APPLICATION NUMBER: US 00/662,276
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
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US-11-266-748A-159453
US-11-266-748A-159453
Squence 159453, Application US/11266748A
Squence 159453, Application US/1266748A
Squence 159453, Application No. US20060134663A1
GENERAL INPORMATION:
APPLICANT: Harkin, Paul
SAPLICANT: Hauligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same
FILE REPREMENT.
SPILE REPREMENT.
STATE OF INVENTION: WHENDER: US/11/266,748A
CURRENT APPLICATION UNMBER: US/11/266,748A
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                                                                                                                                               Sequence 117289, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
APPLICANT: Harkin, Paul APPLICANT: Johnston, Patrick APPLICANT: Mulligan, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.3 SEQ ID NO 117289
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Best Local Similarity 78.8<sup>1</sup>
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-117289
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926 TTAAGTTTTAGGGTACATGTGCACAACGTGCAGGTTTGTTACATATGTATACATGTGCCA 867
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78.8%;
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Best Local Similarity 78.8
Matches 115; Conservative
                                           ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-288898
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CORGANISM: Homo Sapiens
US-11-266-748A-340327
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               LENGTH: 1000
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Pred. No. 1.6e-08;
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PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PELLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
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Best Local Similarity 78.8%;
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; ORGANISM: Homo Sapiens
US-11-266-748A-159453
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STATEMENT IN FORMATION:

APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
ITLE OF INVENTION: Transcriptome Microarray Technology and
ITLE OF INVENTION: Methods of Using the Same
ITLE OF INVENTION: Methods of Using the Same
ITLE OF INVENTION: Methods of Using the Same
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-07-18
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Pred. No. 1.6e-08;
0; Mismatches 31;
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Sequence 3, Application US/10506549
Publication No. US20060100417A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: APPLERA CORPORATION
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUMBER: US/10/506,549
CURRENT APPLICATION NUMBER: US/10/506,549
CURRENT FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 60/361,343
PRIOR APPLICATION NUMBER: 60/361,343
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Pred. No. 1.6e-08;
0; Mismatches 31; Indels
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PATCHIN VERSION 3.3
SEQ ID NOS 483996
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LOCATION: (1)...(394191)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 78.8%;
Matches 115; Conservative
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Best Local Similarity 78.8'
Matches 115; Conservative
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US-11-266-748A-470871
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LENGTH: 394191
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US-11-266.748A-399825/C
Sequence 399825, A9816.2410.0134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319.89)
CURRENT FAPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
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Sequence 470317.0501.
Sequence 470317. Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REPERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT PILING DATE: 2005-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR PLILING DATE: ED04-11-03

PRIOR PLILING DATE: EP 04105479.2
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Best Local Similarity 78.8%; Pred. No. 1.6e-08;
Matches 115; Conservative 0; Mismatches 31;
                 135 TGGTGGTGTGCTGCACCCATTAACTC 160
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US-11-266-748A-399825
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Gaps

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Length 1000;

137007

Length 394191;

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629225 TAAGTITTAGGGTACATGTGCACAATGTGCAGGTTAGTTACATATGTATATATGTATACATGTGCCAT 629166
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                                                                                                                                                                                                                                                                                                                                                                                          Length 755217;
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US-11-266-748A-25123/C

§ Sequence 25123, Application US/11266748A

§ Sequence 25123, Application US/11266748A

§ Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Honston, Parrick

APPLICANT: Muligan, Rarl

TILLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: TRANSCRIPTOM WHERE US/11/266,748A

CURRENT APPLICATION NUMBER: US 0105411-03

FRIOR APPLICATION NUMBER: EP 04105482.6

FRIOR APPLICATION NUMBER: EP 04105482.6

FRIOR FILING DATE: 2004-11-03

FRIOR PELING DATE: 2004-11-03

FRIOR PELING DATE: 2004-11-03

FRIOR APPLICATION NUMBER: EP 04105485.9

FRIOR PELING DATE: 2004-11-03

FRIOR PELING DATE: 2004-11-03

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FRIOR FILING DATE: 2004-11-03

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FRIOR FILING DATE: 2004-11-03

FRIOR FILING DATE: 2004-11-03

FRIOR FILING DATE: 2005-07-01-08
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Pred. No. 3.2e-08;
0; Mismatches 23; Indels
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  PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE. 2004-11-03
PRIOR PLING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
SEQ ID NO 29045
LENGTH: 755217
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 83.4%;
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 483996
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Best Local Similarity 78.2<sup>3</sup>
Matches 115; Conservative
                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo Sapiens
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ORGANISM: Homo Sapiens
US-11-266-748A-25123
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54974 TGTGCACAATGTGCAGGTTAGTTACATATGTATACATGTGCCATGCTGGTGTGCTGCACC 54915
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Pred. No. 2.7e-08;
0; Mismatches 13; Indels 1;
                                                                                                                                                                                                                                                              Sequence 232, Application US/1053928
| Publication No US20060154250A1
| GENERAL INPORMATION:
| APPLICANT: David W. Morris
| APPLICANT: Marc S. Malandro
| TITLE OF INVENTION: Novel Compositions and Methods in Cancer
| FILE REFERENCE: CHIRO052-101 (PP023370.0003)
| CURRENT APPLICATION NUMBER: US/10/539,228
| CURRENT FILING DATE: 2005-06-17
| PRIOR APPLICATION NUMBER: US/10/329,281
| PRIOR APPLICATION NUMBER: US/10/322,281
| PRIOR APPLICATION NUMBER: US/10/322,281
| PRIOR FILING DATE: 2002-12-18
| NUMBER OF SEQ ID NOS: 866
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Miligan, Karl
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
CURRENT APPLICATION UNMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , LOCATION: (1).\(\tilde{\text{.135827}}\)
, OTHER INFORMATION: n = A,T,C or G
US-10-539-228-232
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Best Local Similarity 89.1%;
Matches 115; Conservative (
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                                                                                                                                                                                                                    RESULT 32
US-10-539-228-232/c
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16935 TITAAGITITIAGGIACATGIGCACAATGIGCAGGITAGITACATATGIATACATGIGCC 76876
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APPLICANT: HARTHI, Paul
APPLICANT: HARTHI, Paul
ITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-01-18
PRIOR PILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE PRECEIN VERSION 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 82.4%; Pred. No. 2.2e-08;
Matches 122; Conservative 0; Mismatches 24; Indels 2
                                                                                                                                                                                      76875 ATGCTGGTGCTGCACCGATTAACTC 76849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 ATGCTGGTGTGCTGCACCCATTAACTCA 162
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                                                                                                                                                                                                                                                                                                                   ; Sequence 204505, Application US/11266748A; Publication No. US20060134663A1; GENERAL INFORMATION: APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 60044, Application US/11266748A Publication No. US20060134663A1 APPLICANT: Harkin, Paul APPLICANT: Johnston, Patrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo Sapiens
US-11.266-748A-204505
                                                                                                                                                                                                                                                                           RESULT 35
US-11-266-748A-204505/c
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86731 TATTICACIATIGITIATITICITITITITITICITITITITITITITITITATAC-T
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APPLICANT: HOUSELOW:
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
CURRENT APPLICATION UNDBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
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PRIOR PELING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
TITLE OF INVENTION: Transcriptome Microarray Technology and TITLE OF INVENTION: Methods of Using the Same FILE REFRENCE: 58815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR PAPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR PILING DATE: 2005-01-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-18
NUMBER OF SECTUMER: PACENTIN VERSION 3.3
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Pred. No. 3.4e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.7%;
Best Local Similarity 82.9%;
Matches 121; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo Sapiens
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US-11-266-748A-220785
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525 TTAAGGTTTAGGGTACATGTGCACAATGTGCAGGTTAGTAACATATGTATACATGTGCCA 584
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US-11-266-748A-335897/C

i Sequence 335897/C

i Sequence 335897/C

i Sequence 335897/C

i Sequence 335897/C

i Sequence 335897/C

i GENERAL INFORMATION:

i APPLICAMY: Harthin, Paul

i APPLICAMY: Harthin, Paul

i APPLICAMY: Muligan, Karl

i APPLICAMY: Muligan, Karl

i TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: WHABER: US/11/266,748A

CURRENT APPLICATION NUMBER: EP 04105479.2

FRIOR APPLICATION NUMBER: EP 04105482.6

FRIOR APPLICATION NUMBER: EP 04105483.4

FRIOR APPLICATION NUMBER: EP 04105483.4

FRIOR APPLICATION NUMBER: EP 04105485.9

FRIOR APPLICATION NUMBER: EP 04105485.9

FRIOR PILING DATE: 2004-11-03

FRIOR PILING DATE: 2004-11-03

FRIOR PILING DATE: 2004-11-03

FRIOR PILING DATE: 2004-11-03

FRIOR APPLICATION NUMBER: EP 04105484.2

FRIOR APPLICATION NUMBER: US 60/662,276

FRIOR APPLICATION NUMBER: US 60/700,293

FRIOR PILING DATE: 2005-03-14

FRIOR FILING DATE: 2005-07-18

NUMBER OF SEQ ID NOS: 483996

SOFTWARE PERIOR PILING VARSION 3.3
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Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.6%; Score 95.2; DB 8; Length 1 Best Local Similarity 82.9%; Pred. No. 2.6e-08; Matches 121; Conservative 0; Mismatches 23; Indels
                                                                                                                             585 TGCTGGTGTGCTGCACCCATTAACTC 610
                                                                                                  136 TGCTGGTGTGCTGCACCCATTAACTC 161
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; ORGANISM: Homo Sapiens
US-11-266-748A-335897
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US-11-266-748A-394477
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APPLICANT: Johnston, Patrick
APPLICANT: Muligan, Karl
ITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR RILING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2005-01-10
PRIOR PLING DATE: 2005-01-10
PRIOR PLING DATE: 2005-01-10
PRIOR PLING DATE: 2005-01-10
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR PLING DATE: 2005-07-18
PRIOR PLING DATE: 2005-07-18
PRIOR PLING DATE: 2005-07-18
PRIOR PLING DATE: 2005-07-18
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82.9%; Pred. No. 2.6e-08;
ative 0; Mismatches 23;
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Publication No. US20060134663A1
GENERAL INFORMATION:
PRIOR FILING DATE: 2005-03-14
PRIOR PELICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SEQ ID NO 2207785
LENGTH: 1000
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Best Local Similarity 82.9'
Matches 121; Conservative
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Best Local Similarity 82.9
Matches 121; Conservative
                                                                                                                                                                                  ; ORGANISM: Homo Sapiens
US-11-266-748A-220785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Harkin, Paul
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SEQ ID NO 284468
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                                                                                                                                                               TYPE: DNA
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NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
SEQ ID NO 465523
LENGTH: 1000
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LOCATION: (18413)..(18436)
OTHER INFORMATION: n is a,
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(19594)..(19695)
                                                                                                              TYPE: DNA
CORGANISM: Homo Sapiens
US-11-266-748A-465523
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Best Local Similarity
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LENGTH: 22884
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NAME/KEY:
LOCATION:
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Sequence 465523, Application US/11266748A

Publication No. US20060134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Harkin, Paul

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2005-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR APPLICATION NUMBER: EP 04105483.9

PRIOR PILING DATE: 2004-11-03

PRIOR PELING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

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PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR FILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR PRIOR DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105481.2
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13.6%; Score 95.2; DB 8;
Best Local Similarity 82.9%; Pred. No. 2.6e-08;
Matches 121; Conservative 0; Mismatches 23;
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR PELICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
SRIOR FILING DATE: 2005-03-14
NUMBER OF SEQ ID NOS: 483996
SEQ ID NO 394477
LENGTH: 1000
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APPLICATION NUMBER: US 60/700,293
FILING DATE: 2005-07-18
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CORGANISM: Homo Sapiens
US-11-266-748A-394477
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RESULT 42
US-11-347-766-75/C
US-11-347-766-75/C
; Sequence 75, Application US/11347766
; Publication No. US20060134751A1
; GENERAL INFORMATION:
; APPLICANT: Tedder, Thomas F
; APPLICANT: Liang, Yinghua
; TITLE OF INVENTION: Identification of Novel Gene Family Members Expressed by
; TILE OF INVENTION: Hematopoietic Cells
; FILE REFERENCE: 180/13.2 PCT/US
; CURRENT APPLICATION NUMBER: US/11/347,766
; CURRENT FILING DATE: 2006-02-02
; PRIOR FILING DATE: 2003-09-30
; NUMBER OF SEQ ID NOS: 81
; SOFFWARE: PatentIn version 3.2
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NAME/KEY: genomic_DNA
NAME/KEY: genomic_DNA
NAME/KEY: genomic_DNA
OTHER INFORMATION: 0.1. (22884)
OTHER INFORMATION: n is an undetermined nucleotide (dATP, dCTP, dGTP, or dTTP)
                                                                                                                                                                                                                    Gaps
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Length 1000;
  13.6%; Score 95.2; DB 8; Length 10
82.9%; Pred. No. 2.6e-08;
tive 0; Mismatches 23; Indels
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LOCATION: (9562)..(9621)
OTHER INFORMATION: n is a, c, g,
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LOCATION: (12238)..(12393)
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Sequence 19620, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Karl
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICANT NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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; ORGANISM: Homo Sapiens
US-11-266-748A-60108
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                                                                                                Length 22884;
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APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Miligan, Karl
APPLICANT: Miligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPERENCE: 58815-0102 (319189)
CURRENT APPLICATION WUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR PELLOR DATE: 2004-11-03
PRIOR PELLOR DATE: 2004-11-03
PRIOR APPLICATION WUMBER: EP 04105483.4
PRIOR APPLICATION WUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
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PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION WUMBER: EP 04105484.2
PRIOR APPLICATION WUMBER: US 60/662,276
PRIOR APPLICATION WUMBER: US 60/662,276
PRIOR APPLICATION WUMBER: US 60/700,293
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
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                                                                                           Query Match
Best Local Similarity 83.3°
Matches 120; Conservative
; NAME/KEY: coding region
; LOCATION: (20223)..(20249)
US-11-347-766-75
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US-11-266-748A-25150
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Best Local Similarity
Matches 120; Conserv
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SEQ ID NO 25150
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44 TATCATTTTCTTTTTTTTATTATATACTTTTTAAGTTTTTAGGGTACATGTGCAAAGTG 103
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GENERAL INFORMATION:

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Pred. No. 2.7e-08;
0; Mismatches 60;
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Best Local Similarity 70.0%;
Matches 142; Conservative
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104 TGCAGGTTAGTTACATATATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTCAC 163
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APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Karl
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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13.6%; Score 95; DB 8; Length 81085;
Best Local Similarity 81.9%; Pred. No. 4.2e-08;
Matches 122; Conservative 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                         Length 498;
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Pred, No. 2.7e-08;
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Best Local Similarity 70.0%;
Matches 142; Conservative 0
       PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
SEQ ID NO 239532
LENGTH: 498
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US-11-266-748A-25123
                                                                                                                                                                                                                ; ORGANISM: Homo Sapiens
US-11-266-748A-239532
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LENGTH: 81085
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Sequence 23952/S. Application US/11266748A
Fublication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Kari
ITILE OF INVENTION: Transcriptome Microarray Technology and
ITILE OF INVENTION: Methods of Using the Same
ITILE OF INVENTION: Methods of Using the Same
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
FRIOR PPLICATION NUMBER: EP 04105479.2
FRIOR PPLICATION NUMBER: EP 04105482.6
FRIOR PAPLICATION NUMBER: EP 04105483.4
FRIOR PELING DATE: 2004-11-03
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PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
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PRIOR PILING DATE: 2005-01-14
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PRIOR FILING DATE: 2005-01-14
PRIOR FILING DATE: 2005-01-14
PRIOR PLING DATE: 2005-01-14
PRIOR PLING DATE: 2005-01-18
NUMBER OF SEQ ID NOS: 483996
SEQ ID NO 219620
LENGTH: 498
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APPLICATION NUMBER: US 60/700,293
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Matches 142; Conservative
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; ORGANISM: Homo Sapiens
US-11-266-748A-219620
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TANGO129 AND INTEGRIN ALPHA SUBUNIT PROTEIN
FILE OF INVENTION: DELTA3, JOSE M.

TITLE OF INVENTION: BELLA3, FTHMA-070, TANGO129 AND INTEGRIN ALPHA SUBUNIT
TITLE OF INVENTION: SPOIL, NEOKINE, TANGO129 AND INTEGRIN ALPHA SUBUNIT
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REFERENCE: MPIO5-0100MNIM
CURRENT PLING DATE: 2005-07-05
FRIOR APPLICATION NUMBER: US 10/417,719
FRIOR APPLICATION NUMBER: US 09/568,218
FRIOR APPLICATION NUMBER: US 09/82,855
FRIOR APPLICATION NUMBER: US 09/812,855
FRIOR APPLICATION NUMBER: US 09/812,855
FRIOR PELLING DATE: 1997-06-11
FRIOR PELLING DATE: 1997-06-11
FRIOR PELLING DATE: 1997-04-04
FRIOR APPLICATION NUMBER: US 10/105,934
FRIOR APPLICATION NUMBER: US 10/105,934
FRIOR APPLICATION NUMBER: US 09/862,972
FRIOR APPLICATION NUMBER: US 09/862,972
FRIOR PELLING DATE: 2001-05-22
FRIOR PELLING DATE: 1998-04-17
FRIOR PELLING DATE: 1999-10-10
FRIOR APPLICATION NUMBER: US 60/062,017
FRIOR APPLICATION NUMBER: US 60/062,017
FRIOR APPLICATION NUMBER: US 60/062,017
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                                                                                                                                          135685 CGCCATGCTGCTGCACCCACTAACTC 135715
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Pred. No. 4.5e-08;
0; Mismatches 35;
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                                                                                                 131 TGCCATGCTGGTGTGCTGCACCCATTAACTC
                                                                                                                                                                                                                                                                                                                      Sequence 87, Application US/11175714
Publication No. US20060122373A1
GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-11-175-714-87
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76.8%;
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Mackay, Charles
Lora, Jose M.
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Matches 116; Conservative
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ORGANISM: Homo Sapiens
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APPLICANT: Barnes, Thomas M.
APPLICANT: Mackay, Charles
APPLICANT: Mackay, Charles
APPLICANT: Mackay, Charles
APPLICANT: Lora, Jose M.
TITLE OF INVENTION: DELTA3, FTHMA-070, TANGO85, TANGO77,
TITLE OF INVENTION: SPOIL, NEDKINE, TANGO129 AND INFEGRIN ALPHA SUBUNIT PROTEIN
TITLE OF INVENTION: AND NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REFERENCE: MPIO5-0100MNIM
TITLE OF INVENTION NUMBER: US/11/175,714
CURRENT FILING DATE: 2005-07-05
FRIOR APPLICATION NUMBER: US 10/417,719
FRIOR APPLICATION NUMBER: US 09/568,218
FRIOR APPLICATION NUMBER: US 09/972,855
FRIOR APPLICATION NUMBER: US 10/972,676
FRIOR APPLICATION NUMBER: US 10/985,676
FRIOR PILING DATE: 2004-07-21
FRIOR APPLICATION NUMBER: US 10/105,934
FRIOR APPLICATION NUMBER: US 10/105,934
FRIOR APPLICATION NUMBER: US 09/662,389
FRIOR APPLICATION NUMBER: US 09/662,389
FRIOR APPLICATION NUMBER: US 06/062,017
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                                                                Gaps
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                                                                                                                                                                                                                           19058 CCATGCTGCTGCCACCCACTAACTC 19086
                                                                                                                                                                                         CCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Millennium Pharmaceuticals, Inc. APPLICANT: McCarthy, Sean A.
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 86, Application US/11175714
Publication No. US20060122373A1
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OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McCarthy, Sean A.
Gearing, David
Holtzman, Douglas A.
Pan, Yang
Busfield, Samantha J.
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Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature LOCATION: (1)... (15233
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13.6%; Score 95; DB 8; Length 495475;
Best Local Similarity 76.8%; Pred. No. 5e-08;
Matches 116; Conservative 0; Mismatches 35; Indels 0
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: LOCATION: (448538)..(448538)

: OTHER INDERVATION: n is a, c, g, or t

US-11-266-748A-28223
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LOCATION: (202671)..(202672)
OTHER INFORMATION: n is a, c,
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LOCATION: (202680)..(202680)
OTHER INFORMATION: n is a, c,
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LOCATION: (202691)..(202691)
OTHER INFORMATION: n is a, c,
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NAME/KEY: misc_feature
LOCATION: (202701)..(202702)
OTHER INFORMATION: n is a, c,
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LOCATION: (202712)..(202714)
OTHER INFORMATION: n is a, c,
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LOCATION: (448497)..(448497)
OTHER INFORMATION: n is a, c,
NAME/KEY: misc_feature
LOCATION: (202548)..(202648)
OTHER INFORMATION: n is a, c,
FEATURE:
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NAME/KEY: misc_feature
LOCATION: (202684)...(202684)
OTHER INFORMATION: n is a, c,
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LOCATION: (202586)..(202686)
OTHER INFORMATION: n is a, c,
FEATURE:
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LOCATION: (202696)..(202697)
OTHER INFORMATION: n is a, c,
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NAME/KEY: misc_feature
LOCATION: (448499)..(448500)
OTHER INFORMATION: n is a, c,
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LOCATION: (202663)..(202663)
OTHER INFORMATION: n is a, c,
                                                                                   NAME/KEY: misc feature
LOCATION: (202661)..(202661)
OTHER INFORMATION: n is a, c,
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APPLICANT: HAKKIN, Paul
APPLICANT: HAKKIN, Paul
APPLICANT: Mulligan, Karl
ITLE OF INVENTION: Transcriptome Microarray Technology and
ITLE OF INVENTION: Transcriptome Microarray Technology and
ITLE OF INVENTION: Methods of Using the Same
FILE OF INVENTION: WHORER: US/11/266,748A
CURRENT APPLICATION NUMBER: US 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105486.9
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2005-03-14
PRIOR PLING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE PRILING DATE: 2005-03-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE PRILING DATE: 2005-03-18
  Sequence 28223, Application US/11266748A Ublication No. US20060134663A1 GENERAL INFORMATION:
APPLICANT: Harkin, Paul
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LOCATION: (42263)..(42263)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
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NAME/KEY: misc_feature
LOCATION: (42260) .. (42260)
OTHER INFORMATION: n is a, c, g,
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LOCATION: (42256)..(42256)
OTHER INFORMATION: n is a, c, g,
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LOCATION: (14173)..(14173)
OTHER INFORMATION: n is a, c,
FEATURE:
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LOCATION: (205$2)..(20681)
OTHER INFORMATION: n is a, c,
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NAME/KEY: misc_feature
LOCATION: (14162)..(14163)
OTHER INFORMATION: n is a,
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LOCATION: (21980)..(21980)
OTHER INFORMATION: n is a,
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LOCATION: (21992)..(21992)
OTHER INFORMATION: n is a,
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ORGANISM: Homo Sapiens
                                                                                                               RESULT 50
US-11-266-748A-28223
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LENGTH: 495475
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US-11-266-748A-29045
; Sequence 29045, Application US/11266748A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MS4A12 initial coding_region (91488)..(91760)
                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (32640)..(32640)
OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: misc feature
LOCATION: (104561)..(104625)
OTHER INFORMATION: n is a, c, g, or t
US-11-347-766-79
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(101182)..(101283)
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                                   NAME/KEY: MS4A7 coding region LOCATION: (23741)..(23947)
                                                                                       NAME/KEY: MS4A7 coding region LOCATION: (27037)..(27138)
                                                                                                                                            NAME/KEY: MS4A7 coding region LOCATION: (28139)..(28210)
                                                                                                                                                                                                                                                                                                                          NAME/KEY: MS4A5_coding_region
LOCATION: (65149)..(65277)
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(68118)..(68270)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MS4A5 coding region (82002)..(82109)
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LOCATION: (21068)..(21124)
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FEATURE:
NAME/KEY: I
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LOCATION:
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                          US-11-347-766-79/C

Sequence 79, Application US/11347766

Sequence 79, Application US/11347766

Publication No. US20060134751A1

SENERAL INFORMATION:
APPLICANT: Tedder, Thomas F

APPLICANT: Tedder, Thomas F

TITLE OF INVENTION: Identification of Novel Gene Family Members Expressed by
TITLE OF INVENTION: Hematopoietic Cells
FILE REFERENCE: 180/132 PGT/US

CURRENT APPLICATION NUMBER: US/11/347,766

CURRENT PILING DATE: 2006-02-02

PRIOR FILING DATE: 2003-09-30

NUMBER OF SEQ ID NOS: 81

SSOTHARE: PatentIn version 3.2

SEQ ID NO 79

LENGTH: 104644
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: genomic_DNA
LOCATION: (1)..(104644)
OTHER INFORMATION: n is an undetermined nucleotide (dATP, dCTP, dGTP, or dTTP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc feature
LOCATION: (11699)..(11699)
OTHER INFORMATION: n is a, c, g, or t
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NAME/KEY: MS4A7_initial_coding_region
LOCATION: (17493)..(17639)
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NAME/KEY: misc_feature
LOCATION: (73)..(73)
OTHER INFORMATION: n is a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: (143)..(143)
OTHER INFORMATION: n is a, c,
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LOCATION: (19439)...(19573)
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LOCATION: (1)...(3)
OTHER INFORMATION: n is a, c
FEATURE:
NAME/KEY: misc feature
LOCATION: (39)...(39)
OTHER INFORMATION: n is a, c
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OTHER INFORMATION: n is a,
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LOCATION: (11659)..(11659)
THER INFORMATION: n is a,
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LOCATION: (242)...(242)
OTHER INFORMATION: n is a,
FEATURE:
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LOCATION: (362)..(362)
OTHER INFORMATION: n is a,
FEATURE:
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LOCATION: (231)
OTHER INFORMATION: n is
                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: homo sapiens
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164203 TGTTGGTGTGCTGCACCCATTAACT 164179
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PATCHIN VETSION 3.3
SEQ ID NO 23277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 TGCTGGTGTGCTGCACCCATTAACT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 60144, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin version 3.3 SEQ ID NO 60144 LENGTH: 166949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 483996
                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23277
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US-11-266-748A-60144
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US-11-266-748A-60144
                                                                                                                                                                                                                                                                                                                 LENGTH: 209216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Harkin, Paul
APPLICANT: Honston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
                                                         APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFREENCE: 55815-0102 (319189)
CURRENT APPLICATION UNDER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
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PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 0410550.0
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/602,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
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; Sequence 23277, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
      Publication No. US20060134663A1
GENERAL INFORMAŢION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Homo Sapiens
US-11-266-748A-29045
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LENGTH: 755217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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Length 209216;
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APPLICANT: ASTAIN, PAUL
APPLICANT: Muligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Weehods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
FILE REFERENCE: 55815-0102 (319189)
FILE REFERENCE: 2005-11-03
FRIOR APPLICATION NUMBER: EP 04105482.6
FRIOR APPLICATION NUMBER: EP 04105483.4
FRIOR FILING DATE: 2004-11-03
FRIOR FILING DATE: 2004-11-03
FRIOR APPLICATION NUMBER: EP 04105485.9
FRIOR APPLICATION NUMBER: EP 04105485.9
FRIOR APPLICATION NUMBER: EP 04105484.2
FRIOR APPLICATION NUMBER: EP 04105484.2
FRIOR APPLICATION NUMBER: US 60/662,276
FRIOR APPLICATION NUMBER: US 60/662,276
FRIOR APPLICATION NUMBER: US 60/700,293
FRIOR APPLICATION NUMBER: US 60/700,293
FRIOR APPLICATION NUMBER: US 60/700,293
Query Match
13.5%; Score 94.6; DB 8; Length 20;
Best Local Similarity 82.8%; Pred. No. 5.4e-08;
Matches 120; Conservative 0; Mismatches 24; Indels
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                                                                                                                        16 TTTTTTTTTTGATGATTTTAATAAAATATCATTTTCTTT
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13.5%; Score 94.4; DB 8;
Best Local Similarity 74.4%; Pred. No. 5.7e-08;
Matches 119; Conservative 0; Mismatches 41;
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803 TTTCAACAATCACTCTTTTATTATTATTATTATTATTATAC-TTTAAGTTTTAGGGTACA 745
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; Sequence 23474, Application US/11266748A
; Publication No. US2000134663A1
; GENERAL INFORMATION:
    APPLICANT: Harkin, Paul
    APPLICANT: Harkin, Paul
    APPLICANT: Harkin, Paul
    APPLICANT: Mulligan, Karl
    TITLE OF INVENTION: Methods of Using the Same
    TITLE OF INVENTION: Methods of Using the Same
    TITLE OF INVENTION: WHORER: US/11/266,748A
    TITLE OF INVENTION: WHORER: US/11/266,748A
    FILE REFERENCE: 55815-0102 (319189)
    CURRENT FILING DATE: 2005-11-03
    PRIOR APPLICATION NUMBER: EP 04105479.2
    PRIOR FILING DATE: 2004-11-03
    PRIOR FILING DATE: 2004-11-03
    PRIOR FILING DATE: 2004-11-03
    PRIOR FILING DATE: 2004-11-03
    PRIOR FILING DATE: 2004-11-03
    PRIOR FILING DATE: 2004-11-03
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                                 TITE OF INVENTION: Transcriptome Microarray Technology and TITE OF INVENTION: Transcriptome Microarray Technology and TITE OF INVENTION: Transcriptome Microarray Technology and TITE OF INVENTION: Methods of Using the Same FILE OF INVENTION: WHERE: US/11/266,748A CURRENT APPLICATION NUMBER: US/11/266,748A CURRENT APPLICATION NUMBER: US 04105479.2 PRIOR APPLICATION NUMBER: EP 04105479.2 PRIOR PILING DATE: 2004-11-03 PRIOR PELLING DATE: 2004-11-03 PRIOR APPLICATION NUMBER: EP 04105483.4 PRIOR FILING DATE: 2004-11-03 PRIOR PELLING DATE: 2004-11-03 PRIOR PELLING DATE: 2004-11-03 PRIOR PELLING DATE: 2004-11-03 PRIOR PELLING DATE: 2004-11-03 PRIOR PELLING DATE: 2004-11-03 PRIOR PELLING DATE: 2004-11-03 PRIOR PELLING DATE: 2004-11-03 PRIOR FILING DATE: 2004-11-03 PRIOR PELLING DATE: 2004-11-03 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING DATE: 2005-01-18 PRIOR FILING PRIOR FILING PRIOR FILING PRIOR FILING PRIOR FILING PRIOR FILING PRIOR FILING PRIOR FILING PRIOR FILING PRIOR FILING PRIOR FIL
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Pred. No. 4.3e-08;
0; Mismatches 15; Indels
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Best Local Similarity 87.7%;
Matches 114; Conservative
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US-11-266-748A-202832
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                                                                                                                                                                                                                              189 ACTITIAAGITCTAGGGTACATGTGCACAACGTGCAGGTTTGTTACATATGTATACATGT 248
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GENERALI INFORMATION:
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REPERRORE: 58815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PELLING DATE: 2004-11-03
PRIOR PELLING DATE: 2004-11-03
PRIOR PELLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PELLING DATE: 2004-11-03
PRIOR PELLING DATE: 2004-11-03
PRIOR PELLING DATE: 2004-11-03
PRIOR PELLING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR PELLING DATE: 2005-03-14
PRIOR PELLING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PELLING DATE: 2005-03-14
PRIOR PELLING DATE: 2005-03-14
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                                                                                                                                                                                                                                                                                                                                                                                                         19760 GTATACATGTGCCATGCTGGTGCGCTGCACCACTAACTC 19799
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0; Mismatches 35
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; Sequence 202832, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 50139, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
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Best Local Similarity 76.73
Matches 115; Conservative
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; ORGANISM: Homo Sapiens
US-11-266-748A-50139
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LOCATION: (3392)..(3392)
OTHER INFORMATION: n is a,
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LOCATION: (3907)..(390
           misc_feature
(3392)..(339
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APPLICANT: HARTH, Paul
APPLICANT: HARTH, Paul
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PELING DATE: 2004-11-03
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PRIOR PLING DATE: 2005-01-16
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PRIOR FILING DATE: 2005-01-18
PRIOR FILING DATE: 2005-01-18
                                                                                                                                                                                                                                                                                                                              Query Match 13.4%; Score 93.8; DB 8; Length 3 Best Local Similarity 83.7%; Pred. No. 7.8e-08; Matches 118; Conservative 0; Mismatches 22; Indels
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR PLLING DATE: 2005-03-18
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SSCYWARE: Patentin version 3.3
SEQ ID NO 23474
LENGTH: 347503
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US-11-266-748A-23170
; Sequence 23170, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (3384)..(3384)
OTHER INFORMATION: n is a, c, g, or t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 GTGTGCTGCACCCATTAACTC 161
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LOCATION: (3381)..(3381)
OTHER INFORMATION: n is a,
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US-11-266-748A-23474
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ORGANISM: Homo Sapiens
FEATURE:
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LENGTH: 170452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc_feature
; LOCATION: (144156)..(144156)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-7488-23170
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LOCATION: (3927)..(3927)
OTHER INFORMATION: n is a, c,
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LOCATION: (3423)..(3423)
OTHER INFORMATION: n is a, c,
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LOCATION: (3406)..(3407)
OTHER INFORMATION: n is a,
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LOCATION: (3446)..(3446)
OTHER INFORMATION: n is a,
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LOCATION: (3545)..(3545)
OTHER INFORMATION: n is a,
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LOCATION: (3905)..(3905)
OTHER INFORMATION: n is a,
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LOCATION: (390<u>9</u>)..(3909)
OTHER INFORMATION: n is a,
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LOCATION: (3922)..(3922)
OTHER INFORMATION: n is a,
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LOCATION: (3924)..(3924)
OTHER INFORMATION: n is a,
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LOCATION: (15605)..(15605)
OTHER INFORMATION: n is a,
NAME/KEY: misc feature
LOCATION: (3400)..(3400)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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; NAME/KEY: misc_feature
; LOCATION: (24475)..(24476)
UCHER INFORMATION: n is a, c, g, or
US-11-266-748A-6080a
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Matches 118; Conservative
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CORGANISM: Homo Sapiens
US-11-266-748A-200176
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ORGANISM: Homo Sapiens
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Publication No. US20060134663A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICANT NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 13.3%; Score 93.4; DB 8; Length 1 Best Local Similarity 86.6%; Pred. No. 1e-07; Matches 103; Conservative 0; Mismatches 16; Indels
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PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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US-11-266-748A-29041
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LENGTH: 1237661
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SEQUENCE 60003, Application US/11266748A

Publication No. US20060134663A1

SEQUENCE INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Johnston, Patrick

APPLICANT: Johnston, Patrick

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: Methods of Using the Same

TITLE OF INVENTION: Methods of Using the Same

TITLE OF INVENTION: Methods of Using the Same

TITLE OF INVENTION: Methods of Using the Same

TITLE OF INVENTION: Methods of Using the Same

CURRENT FILING DATE: 2004-11-03

PRIOR PELING DATE: 2004-11-03

PRIOR PELING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR PELING DATE: 2004-11-03

PRIOR PELING DATE: 2004-11-03

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PRIOR PELING DATE: 2005-07-18

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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: Patentin version 3.3
SEQ ID NO 200176
LENGTH: 1000
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                                                                       1; Gaps
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Score 93.2; DB 8; Length 176928; Pred. No. 9.3e-08; 0; Mismatches 33; Indels 1;
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US-11-266.748A-29039
US-11-266.748A-29039
US-11-266.748A-29039
US-11-266.11 NFORMATION:
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Walligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
UNRENT APPLICATION NUMBER: ED 0410549.2
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
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PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
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Pred. No. 1.1e-07;
0; Mismatches 33;
Query Match
Best Local Similarity 78.5%;
Matches 124; Conservative
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Best Local Similarity 78.1%;
Matches 125; Conservative
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US-11-266-748A-29039
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RESULT 63 US-11-266-748A-211402

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APPLICANT: Cavarec, Laurent APPLICANT: Chumakov, Ilya APPLICANT: Chumakov, Ilya APPLICANT: Chumakov, Ilya APPLICANT: Chumakov, Ilya APPLICANT: Gatherine APPLICANT: Gatherine APPLICANT: Gatherine APPLICANT: Elias, Isabelle TITLE OF INVENTION: TRAGATWENT OF MENTAL DISORDERS FILE OF INVENTION: TRAGATWENT OF MENTAL DISORDERS FILE REFERENCE: G-1940X03PCT CURRENT APPLICATION NUMBER: US/10/519,335
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 60/391,359
PRIOR APPLICATION NUMBER: US 60/391,359
PRIOR PILING DATE: 2002-06-25
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 37
LENGTH: 151830
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H
Sequence 211402, Application US/11266748A

Publication No. US20060134663A1

SGENERAL INPORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Harkin, Paul

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: Transcriptome Microarray Technology and

TITLE OF INVENTION: Methods of Using the Same

TITLE OF INVENTION: Methods of Using the Same

TITLE OF INVENTION: WHERE: 2005-11-03

FURENT FILING DATE: 2005-11-03

PRIOR APPLICATION NUMBER: EP 04105479.2

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR PELLING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR FILING DATE: 2004-11-03

PRIOR PELLING DATE: 2004-11-03

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PRIOR PELLING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2004-11-03

PRIOR FILING DATE: 2006-01-03

PRIOR FILING DATE: 2006-01-03

PRIOR FILING DATE: 2005-03-14

PRIOR FILING DATE: 2005-03-14

PRIOR FILING DATE: 2005-07-18

NUMBER OF SEQ ID NOS: 483996

SOFTWARE PALEACTIN VERSION 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 607;
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Pred. No. 6.1e-08;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 13.3%;
Best Local Similarity 94.7%;
Matches 107; Conservative
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
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US-11-266-748A-211402
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LENGTH: 607
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NAME/KEY: misc feature
LOCATION: (56012)..(56012)
OTHER INFORMATION: n = a or c or g or
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LOCATION: (143077)..(143077)
OTHER INFORMATION: n = a or c or g or
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LOCATION: (10296)..(10296)
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NAME/KEY: misc_feature
LOCATION: (16397)..(16397)
OTHER INFORMATION: n = a or c or g or
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LOCATION: (15336)..(15336)
OTHER INFORMATION: n = a or c or g or
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LOCATION: (149079)..(149079)
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LOCATION: (8080)..(8080)
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MANG/KEY: misc feature
LOCALION: (14528)
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NAME/KRY: misc_feature
NACATION: (142967).
OTHER INFORMATION: n = a or c
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         OTHER INFORMATION: n = a or c
                                            NAME/KEY: misc feature
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LOCATION: (98210) ..(98210)
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LOCATION: (10)...(10)
OTHER INFORMATION: n = a or c or g or t
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LOCATION: (98208)..(98208)
OTHER INFORMATION: n = a or c or g or
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LOCATION: (98211)..(98211)
OTHER INFORMATION: n = a or c or g or
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LOCATION: (109125)..(109125)
DTHER INFORMATION: n = a or c or g or
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LOCATION: (118900)..(118900)
OTHER INFORMATION: n = a or c or g or
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LOCATION: (141674)..(141674)
OTHER INFORMATION: n = a or c or g or
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LOCATION: (98209)..(98209)
OTHER INFORMATION: n = a or c or g or
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LOCATION: (119123) .. (119123)
OCHER INFORMATION: n = a or c or g
PEATURE:
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LOCATION: (109094)..(109094)
THER INFORMATION: n = a or c or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (119024)..(119052)
OTHER INFORMATION: n = a or c or
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LOCATION: (119053)..(119112)
JTHER INFORMATION: n = a or c or
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LOCATION: (142063)..(142063)
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APPLICANT: Johnston, Parrick
APPLICANT: Johnston, Parrick
APPLICANT: Johnston, Parrick
APPLICANT: Johnston, Parrick
TITLE OF INVENTION: Methods of Using the Same
FILE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 5815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
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PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR PILING DATE: 2005-03-14
PRIOR PELING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SEQ ID NO 59086
LENGTH: 168545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 22833, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
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US-11-266-748A-22833
                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-59086
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VES-11-266-748A-59086/C

Sequence 59086. Application US/11266748A

Publicanton No. US20660134663A1

GENERAL INFORMATION.

APPLICANT: Harkin, Paul

TITLE OF INVENTION: Wethods of Using the Same

FILE OF INVENTION: Methods of Using the Same

FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT FILING DATE: 2006-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR PILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR APPLICATION NUMBER: EP 04105483.4

PRIOR APPLICATION NUMBER: EP 04105507.0

PRIOR APPLICATION NUMBER: EP 04105507.0

PRIOR PILING DATE: 2004-11-03

PRIOR PAPLICATION NUMBER: EP 04105507.0

PRIOR PAPLICATION NUMBER: EP 04105485.9

PRIOR PILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105485.9

PRIOR PILING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105485.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 13.3%; Score 93; DB 6; Length 151830; Best Local Similarity 77.6%; Pred. No. 1e-07; Matches 125; Conservative 0; Mismatches 35; Indels 1
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                                   NAME/KEY: misc feature
LOCATION: (57662)..(57662)
OTHER INFORMATION: n = a or c or g or
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LOCATION: (96310)..(96422)
OTHER INFORMATION: exon 4
FEATURE:
NAME/KEY: exon
LOCATION: (99546)..(99723)
OTHER INFORMATION: exon 5
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LOCATION: (125441)..(125605)
                                                                                                                                                            NAME/KEY: S'UTR
LOCATION: (1)..(54)
OTHER INFORMATION: exon 1
FEATURE:
NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: exon
LOCATION: (91147)..(91244)
OTHER INFORMATION: exon 2
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OTHER INFORMATION: exon 3
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OTHER INFORMATION: exon 1
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SOFTWARE: PatentIn version 3.3
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Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-11-266-748A-25022
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                                                        61651 CTGTCCGCAAAAACATTCTTTTTTTTTTTTGGTCTTTATTATTATTATTATTATTATTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 TIATTATAC-TITAAGTITITAGGGTACATGTGCACAATGTGCAGGTTAGTTACATATGTA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 TTTAAACATTTTGATGTATTTTAATACAGGGTAGTTATTGTTCTTTTTTTAATTTTTATTA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 TICACATAAAGTITITITITITIGAIGATITITAATAAAATAICATITITITITITATTA
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APPLICANT: ACTAIN, FAUL
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (1319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
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PRIOR FILING DATE: 2005-01-18
PRIOR FILING DATE: 2005-01-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR FILING DATE: 2005-07-18
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR APPLICATION VUMBER: US 60/700,293
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                                                                                                                                                                                                                 61770 TGTATACAGGTGCCATGATGGTGTGCTGCATCCATTAACTC 61810
                                                                                                                                                                            TATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 92.8; DB 8;
Pred. No. 6.9e-08;
0; Mismatches 32;
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 200842, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25022, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION: Paul APPLICANT: Harkin, Paul APPLICANT: Mulligan, Karl
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78.8%;
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Best Local Similarity 78.8'
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-200842
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US-11-266-748A-25022
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| TITLE OF INVENTION: Transcriptoms Microarray Technology and CURRENT PILLS DETRIBUTION: Transcriptoms Microarray Technology and CURRENT PILLS DATE: 2002-11-03
| FILLS PERSONANCE: 55518-101/1666, 44a |
| CURRENT PILLS DATE: 2002-11-03 |
| FILLS PERSONANCE: 2002-11-03 |
| FILLS PERSONANCE: 2002-11-03 |
| FILLS DATE: 2002-11-03 |
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19-11-266-748A-60803/C

Sequence 60803, Application US/11266748A

Publication No. US20600134663A1

GENERAL INFORMATION:

APPLICANT: Harkin, Paul

APPLICANT: Mulligan, Karl

TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same

TITLE OF INVENTION: NUMBER: US/11/266,748A

CURRENT APPLICATION NUMBER: EP 04105479.2

PRIOR PELING DATE: 2004-11-03

PRIOR PELING DATE: 2004-11-03

PRIOR APPLICATION NUMBER: EP 04105482.6

PRIOR PLING DATE: 2004-11-03

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13.2%; Score 92.6; DB 8; Length 176928;
Best Local Similarity 82.5%; Pred. No. 1.2e-07;
Matches 118; Conservative 0; Mismatches 24; Indels 1;
                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                               Query Match
13.2%; Score 92.6; DB 8; Length 39638;
Best Local Similarity 72.7%; Pred. No. 1e-07;
Matches 133; Conservative 0; Mismatches 49; Indels 1;
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| LOCATION: (24475)..(24476)
| OTHER INFORMATION: n is a, c, g, or t
| US-11-266-7488-60803
; SEQ ID NO 23809
; LENGTH: 39638
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-23809
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Run on:

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BX415806 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP008YE09 3-PRIME, mRNA sequence.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 961)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
Unpublished (2001)
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CR750736
AF118407
AQ464599
CZ465237
                                             AA344409
CA947015
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BS2311 CIT-HSP-388
AQ356702 CITBI-E1-AQ195233 RPCI11-48
BB349127 BB349127
AQ181354 CIT-HSP-2
CX669873 HESC4 38
DA104597 DA104597
AQ184211 HS 5499 B
AQ102621 PRI LYOGI
AQ257159 CITBI-E1-W44804 Zb98909.51
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CR737970 CR737970
AQ021610 CIT-HSP-2
CZ6511937 NISC_G101
                                            July 19, 2006, 06:54:08; Search time 4403 Seconds (without alignments) 8890.196 Million cell updates/sec
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       GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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                                                                                                                    48236798 segs, 27959665780 residues
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B52311 522 bp DNA linear GSS 20-JUN-1998 CIT-HSP-388D1.TR CIT-HSP Homo sapiens genomic clone 388D1, genomic
                                                                                                                                                                                                                                                     /note="Vector: pECBAC1; Site_1: HindIII; This library was constructed from MCF7 breast_cancer cell line by Amplicon Express (http://www.genomex.com) using their standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    455 TGCTGGTGTGCTGCACCCATTAACTGTCATTTAAGCATTACAAAATTTCTTAACCTTT 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 TGCTGGTGTGCTGCACCCATTAACTCACATGAAGTTTTTTTAAATTTTAGTGACAGTTT 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: M13 Reverse
Class: BAC ends.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Goldan, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M. and Venter, J.C.
Simon, M. and Venter, J.C.
Building
Unpublished (1997)
                                                                                                                                                                                             /clone_lib="Human MCF7 breast cancer cell line library (MCF7 ])"
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdddams@tigr.org
                                                               1. .785
/organism="Homo sapiens"
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  http://www.genomex.com
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Matches 138; Conservative
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                     Class: BAC ends
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              Contract: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, IV Web: www.genoscope.cns.fr
1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime
end enricheed, double-serrand cDNA was digested with Not I and Cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 1683.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CSOCAP008ACOSNP1&c=1683.f.
                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOCA-POOSYE09"
/clone="Type="THYMUS"
/clone="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORY sites of the pCMVSPORT 6 vector. Library was not normalized."
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BZ598311.1 GI:31506773
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1 (bases 1 to 785).

Volik, S., Zhao, S., Chin, K., Brebner, J.H., Herndon, D.R., Tao, Q., Kowbel, D., Huang, G., Lapuk, A., Kuo, W.-L., Magrane, G., de Jong, P., Gray, J.W. and Collins, C.

End-sequence profiling: Sequence-based analysis of aberrant genomes Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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May 15, 2003 this sequence version replaced gi:30765544.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 15.7%; Score 110; DB 4; Length 961; Best Local Similarity 83.6%; Pred. No. 1.5e-09; Matches 122; Conservative 2; Mismatches 22; Indels
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AQ195233 632 bp DNA linear GSS 20-APR-1999
RPCIl1-48C19.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-48C19,
                                                                                                                                                                                                                                                                             121 TTAAGTTTTTAGGGTACATGTGCACAACGTGCAGGTTTGTTACATATGTATACATGTGCCA 180
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1 (bases 1 to 632)

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
Other GSSs: RPCIII-48C19.TK
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fex: 301 838 0208
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/clone lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIll Human Male BAC Library"
                                                                                                                                                    Length 375;
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                                                                                           27; Indels
                               Score 102.8; DB 11;
Pred. No. 3e-08;
                                                                                           0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                  136 TGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                 181 TGTTGGTGTGCTGCACCCATTAACTC 206
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AQ195233.1 GI:3606845
                                  14.7%;
81.5%;
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                                                                                        Matches 119; Conservative
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                                                               Similarity
                               Query Match
                                                                  Best Local
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1 (bases 1 to 375)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
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Other GSSs: CITBI-E1-2531H1.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0200
Fax: 301 838 0200
Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Contact Con
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Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
Map Building
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Seg primer: M13 Reverse
Class: BAC ends.
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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/clone_lib="CTMBI-B1"
/note="Vector: pBelobAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                          /cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                  DB 11; Length 522;
                                                                                                                                                                                                                                                                                                                                                               Score 106.8; DB 11; Length
Pred. No. 5.8e-09;
0; Mismatches 17; Indels
'organism="Homo sapiens"
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/organism="Homo sapiens"
                            /mol_type="genomic_DNA"
/db_xref="GDB:5379775"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370 TGCTGGTGTGCTGCACCCATTAACTC 395
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/db_xref="taxon:9606"
/clone="2531H1"
                                                                                  /db_xref="taxon:9606"
/clone="388D1"
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                                                                                                                                                                                                                                                                                                                                                         15.3%;
                                                                                                                                                    sex="Male"
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                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 87.77
Matches 128; Conservative
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CX869873.1 GI:58553047
                                                                            AQ111354.1 GI:3488011
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Best Local Similarity 77.8%;
Matches 123; Conservative (
                                                                                                                       Homo sapiens (human)
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CX869873
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FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3975
Fax: 81-438-52-3986
Email: flj-cdha@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB
Location/Qualifiers
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Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Yamashita, R., Yamamoto, J., Sekine, M., Teuritani, K., Wakaguri, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
                                                                                                                                                                                                                         DB349127 TRACH3 Homo sapiens cDNa clone TRACH3005808 3', mRNA
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                     TTATACTITITAAGITITTAGGGTACATGTGCAAAGTGTGCAGGTTAGTTACATATATAC 127
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                        421 ATGTGCCATGCTGGTGCACTGCACCATCTATTCCCCT 458
                                                                                 128 ATGTGCCATGCTGTGTGCTGCACCCATTAACTCACAT 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="trachea"
/clone_lib="TRACH3"
/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                           DB349127.1 GI:83258349
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Matches 108; Conserv
                                                                                                                                                                                                                                                                      sequence.
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AUTHORS
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PUBMED
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DB349127
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RESULT 7 AQ111354

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CX869873 506 bp mRNA linear EST 03-FEB-2005 HESC4 38 E04.gl A037 NIH MGC 262 Homo sapiens cDNA clone IMAGE:7474642 57, mRNA sequence.
AQ111354 197 bp DNA linear GSS 29-AUG-1998
CIT-HSP-2382A15.TR CIT-HSP Homo sapiens genomic clone 2382A15,
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Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
Other GSSs: CIT-HSP-2382A15.TF
Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                    1 (bases 1 to 397)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 iticirrirririririririririririririririri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="Sperm"
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HindIII"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 102; DB 11;
Pred. No. 4.1e-08;
0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="2382A15"
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KEYWORDS
SOURCE
ORGANISM
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Hominidae; Homo.

I (baees 1 to 552)

Yamashita, Rawarsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Wakamatsu, A., Sekine, M., Tsuritani, K., Wakaguri, H., Samashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Genome Res. 16 (1), 55-65 (2006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: flj-cdna@nifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS 09-NOV-1999
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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 421)
                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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HS_5499_B1_G04_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=9267 Col=7 Row=N, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Gaps
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2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 85.6%; Pred. No. 4e-08;
Matches 125; Conservative 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue type="cerebellum"
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/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLJ Project (HRI Team)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
Homo sapiens
                           sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .552
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                                                      ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="embryonic stem"
/cell type="human embryonic stem cells"
/cell type="human embryonic stem cells"
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/note="weetor: pExpress-1; Site_1: Not1; Site_2: EcoRV;
/note="weetor: perspectation coll mass of blastocyst stage embryos and the inner cell mass of blastocyst stage embryos and differentiated to an early neural progenitor cell type.
/cell line id and NIH Registry designation is BGO1.
Positive for Nestin and Musashi expression. Passage number
                                                                                                              Contact: Daniela S. Gerhard, Ph.D.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rml0A07 Betheada, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Bresaden, Inc.

CDNA Library Preparation: Express Genomics, Inc.

CDNA Library Preparation: Express Genomics and Bioinformatics,

University of Georgia

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: LLAM15783 row: i column: 08

Seq primer: JERREY (CAGGAAACAGCTATGACC)

High quality sequence stop: 506.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18. CDNA primed using oligo-dT primer:
5'-pGACTAGTTCTAGATGCGAGGGCGCCCC(T)25-3' and cloned into
the ECORV/NoI sites of pExpress-1. This primary library
is non-normalized (normalized primary library is
NIH_MGC 259). It was constructed by Express Genomics
(Frederick, MD). Sequence ends have been trimmed to
exclude vector and regions below Phred quality 16. Note:
this is a Mammalian Gene Collection library."
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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14.6%; Score 102; DB 9; Length 506;
Best Local Similarity 85.6%; Pred. No. 4.1e-08;
Matches 125; Conservative 0; Mismatches 20; Indels
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DA104597.1 GI:78759434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                 Unpublished (1999)
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TITLE
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PRIMERS
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AQ527159
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                                                                                                                           Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-38618
Fax: (206) 616-38618
Email: jwallacedu, washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Seq primer: 9267 row: N column: 7
Seq primer: 8P66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /notes_Wector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites."
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 TITITATITGTTATTATTATATACTTTTAAGTTTTTAGGGTACATGTGCACAAIGTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 ITTICTTTTTTTATTATTATTATACTTTTAAGTTTTAGGGTACATGTGCAAAGTGTGCAG
                                                         Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Taylor, T.D., Yada, T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.5%; Score 101.8; DB 11; Length 421;
llarity 93.8%; Pred. No. 4.5e-08;
Conservative 0; Mismatches 7; Indels 0;
                                                                    scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .421
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="texon:9606"
/clone="Plate=9267 Col=7 Row=N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: BAC ends
High quality sequence stop: 421.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes (chimpanzee)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 681)
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es 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS.
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Matches
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REFERENCE
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AG102621
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  AUTHORS
                                                                                                                     PUBMED
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                                                                                                 JOURNAL
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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Genomic Sciences 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp, Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ527159 591 bp DNA linear GSS 18-MAY-1999 CITBI-E1-260411.TF CITBI-E1 Homo sapiens genomic clone 260411, genomic survey sequence.
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Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and
Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239
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Seg primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 101.8; DB 14; Length
Pred. No. 4.3e-08;
0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 TTTTTTTTTGATGATTTTTAATAAATATCATTTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1..681
/organism="Pan troglodytes"
/mol_type="genomic_DNA"
/db_xref="taxon:9598"
/clone="PTB-105P19.F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 GCTGGTGTGCTGCACCCATTAACTC 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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AQ527159.1 GI:4838919
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Best Local Similarity 81.4%;
Matches 118; Conservative
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R.Site 1
R.Site 2
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Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                121; Conservative
                                                                                                                                                                                                                                                                                                                             Similarity
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Best Local S
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AQ756779
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W44804 Soares_parathyroid_tumor_NDHPA Homo sapiens CDNA clone IMAGE:320896 3' similar to contains_L1.t3 L1 repetitive element ;,
                                                                                                                                                                                                                                                                                                                                              /cell_type="sperm"
/clone_lib="CITBI-E1"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
                                                                                                                                                                                                                                                                                                                             75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                          16 TITITITITITATAATAAAATAICAITITICATITATIATIATAATAACTI
                                                                                                                                                                                                                                                                                          Gaps
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1 (bases 1 to 242)

1 (bases 1 to 242)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultar,L., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                  14.5%; Score 101.4; DB 11; Length 591; 81.8%; Pred. No. 5.1e-08; tive 0; Mismatches 26; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:320896"

ftissue type="parathyroid tumor"

/dev_stage="adult"

/lab_host="DHIOB (ampicillin resistant)"
              Location/Qualifiers
1. 591
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1258554"
/db_xref="taxon:9606"
                                                                     /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="260411"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: mob.REGA+ET
High quality sequence stop: 233.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 TGCTGGTGCTGCACCCATTAA 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                           /sex="male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                        Conservative
BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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                                                                                                                                                                                                                                                                     Similarity
Class:
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                                                                                                                                                                                                                                                                                  Matches 117;
                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                         Local
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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JOURNAL
COMMENT
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                FEATURES
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieteracedejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                TTTTT-3'), double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and Coloned into the Not I and Eco RI sites of a modified pTTT3 vector (Pharmacia). Library went through one round opportation to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from sportadic parathyroid adenomas was kindly provided by Dr. Stephen Marx, National Institute of Diabetes and Digestive and Kidney Diseases, NIH."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hominidae; Homo.
1 (Boses 1 to 527)
wahairas G.G., wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 CAGTAAGATTTTTATTTTTTTTTTTTTTTTTTTTCCTTTAATTTTTATTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ756779 15.7 AZ G12 T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=983 Col=24 Row=M, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 CATGTGCCATGCTGGTGCGCTGCACCAATTAACTC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          127 CATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 101.2; DB 10
Pred. No. 5.9e-08;
0; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: BAC ends
High quality sequence stop: 527.
Location/Qualifiers
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Seg primer: T7
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GSS.
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78.1%;
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CR137970 Homo sapiens library (Ebert L) Homo sapiens cDNA clone IMAGP98C11359; IMAGE:190402 5', mRNA sequence.
constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             312 TITITITITATAATITAAGITITIAGGGTACATGTGCACATITITGCAGGTTAGTTACATAT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                   2 IGTITCACATAAAGTITITITITITITGATGATITITAATAAAATAICATITITITITA
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                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Hel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998C11359 ; IMAGE:190402"
/clone_lib="Homo sapiens library (Ebert L)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                  37; Indels
                                                                                                                                                                                                                                                                                                                                                                            14.4%; Score 100.8; DB 8; 83.8%; Pred. No. 6.5e-08; ive 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: www.rzpd.de
Exrb: InAcpo98C11359.
RZPDLIB; I.M.A.G.E. CDNA Clone Collection;
Contact: Inge Arlart
                                                                                                                  Score 100.8; DB 1
Pred. No. 6.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 746)
Ebert, L., Heil, O., Hennig, S., Korn, B.,
Peters, M., Radelof, U. and Schneider, D.
I.M.A.G.E. CDNA Clone Collection
Unpublished (2004)
                                                                                                                                                               0; Mismatches

    .746
    /organism="Homo sapiens"

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                                                                                                                       14.48;
76.98;
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                                                                                                                                                                  Matches 123; Conservative
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Matches 114; Conservative
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Best Local Similarity
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JOURNAL
COMMENT
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CR737970
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                             /organism="Homo sapiens"
/mol type="genomic DNA"
/mol type="genomic DNA"
/db xref="taxon:9606"
/clone="Plate=983 Col=24 Row=M"
/sex="male"
/clone="lb="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site 1: EcoR1; Site 2: EcoR1;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoR1 and EcoR1 Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoR1 sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae, Homo.

1 (bases 1 to 445)
Voliks.V., Raphael, B.J., Huang, G.-Q., Murnane, J., Brebner, J.H.,
Bajsarowicz, K., Paris, P., Tao, Q., Kowbel, D., Lapuk, A.V., Kuo, W.-L.,
Shagin, D.A., Shagina, I.A., Magrane, G., Gray, J.W., Jan, F.-C., de
Jong, P., Pevrane, P. and Collins, C.

Decoding the genomic architecture and high throughput detection of
fusion transcripts in breast cancer cell lines: implications for a
tumor genome project
Unpublished (2005)
Contact: Volik SV
Colin Collins' lab
                                                                                                                                                                                                                                                                                                                                                               ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TITIATNNITITATITITATITITAATITITIAAATITITIAAAATITITAAAAATITITAATITITA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CZ457195

WGF740G1ITR Human MCF7 breast cancer cell line library (MCF7 1)
HOmo sapiens genomic clone MCF7_40_G11, genomic survey sequence.
CZ457195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Human MCF7 breast cancer cell line library (MCF7_1)"
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                      DB 11; Length 527;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 GTATACATGTGCCATGCTGGTGTGTATACCCATTAACTC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 ATATACATGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
http://www.genomex.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UCSF Comprehensive Cancer Center UCSF Box 0808, San Francisco, CA 94143-0808, Fal: 415 502 7066 Fax: 415 502 5665
                                                                                                                                                                                                                                                                                                                    Score 101.2; DB 11;
Pred. No. 5.6e-08;
0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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/db_xref="taxon:9606"
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/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 80.6%;
Matches 129; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
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VERSION
KEYWORDS
SOURCE
ORGANISM
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CZ457195
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AUTHORS
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COMMENT
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DEFINITION

ACCESSION

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

RESULT 17 AQ021610

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/dev_stage="adult"
/lab_host="pH10B"
/lab_host="pH10B"
/clone_lib="NCI_CGAP_Pr28"
/clone_lib="Organ: Discrete; Vector: pT7T3D-PacI; Plasmid DNA from the normalized library NCI_CGAP_Pr22 was prepared, and sc circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonelDs 988608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. "Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLML
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
info@limage.llnl.gov
Plate: LLAM8007 row: L column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     233 bp mRNA linear EST 24-MAR-2003 NISC_nclla06.yl COGENE 6E MAX Homo sapiens cDNA clone IMAGE:5776426 5', mRNA sequence. CB410332 GE-10332 1 GI:29167072 EST.
       CB048927 225 bp mRNA linear EST 17-JAN-2003
NISC gj07f10.y1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3271074
5., mRNA sequence.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                               Hominidae, Homo.

1 (bases 1 to 225)

Nor-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

CDNA Library Preparation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 14.3%; Score 100.4; DB 4; Length 225; Best Local Similarity 84.9%; Pred. No. 8.1e-08; Matches 124; Conservative 0; Mismatches 21; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 TITITITITITGATGATTTTAATAAATATCATTTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: LLAW8007 row: L column: 19
Seg primer: M13RP1 reverse primer (ABI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:3271074"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
                                                                                             CB048927.1 GI:27787214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sex="male"
                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                     Homo sapiens
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DEFINITION
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CB410332/c
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Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

Unpublished (1998)

Unpublished (1998)

Contact: Mark Adams

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The Institute for Genomic Research

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Fax: 301 838 0200

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC end search pages
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                                                                                                                                                                                                                                    GSS 09-JUN-1998
318 AGGTTACATGCGCACAATGTGCAGGTTTGTTACATATGTATACATGTGCATGTTGGTGT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: Ml3 Reverse
Class: BAC ends.
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                                                                                                                                                                                                                               AQ021610 417 bp DNA linear GSS 09-JUJ
CIT-HSP-2311P19.TR CIT-HSP Homo sapiens genomic clone 2311P19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Sperm"
/clone lib="CIT-HSP"
/noce="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII
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Pred. No. 7.3e-08;
0; Mismatches 29; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DN/
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                          genomic survey sequence.
                                                                                             378 GCTGCACCCATTAACT 393
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GSS.
                                                                        145 GCTGCACCCATTAACT 160
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Best Local Similarity 81.1%;
Matches 129; Conservative 0
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Homo sapiens
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FEATURES

RESULT 18 CB048927/c

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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
                                                                                                                                                                                                                                                                                                                                                                                                   1. .285
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TGCTGGTGCTGCACCCATTAACTC 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 TGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 285.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                           Clone distribution: NOI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Plate: LLAM12849 row: B column: 11
Seq primer: M13RP1 reverse primer (ABI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=_vector: pAMPI; cDNA primed using oligo-dT primer, directionally cloned into UDG sites of pAMPI. Size selected for insert sizes ranging from 0.2-1.8 kb.
Normalized to Cot5. Primary library, non-amplified.
Library constructed by M. Lovett. For more information on University) or visit the COGENE website at http://hg.wustl.edu/COGENE website at
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 285)
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HS_2033_A2_F09_T7_CIT_Approved Human Genomic Sperm Library D Homo
Bapiens genomic clone Plate=2033 Col=18 Row=K, genomic survey
                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                           Hominidae; Homo.

1 (bases 1 to 23)

NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/nciogap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
cDNA Library Arrabe by: The I.M.A.G.E. Consortium/LLNL
Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="IMAGE:5776426"
/tissue_type="maxilla, pooled"
/dev grage="6 weeks postconception"
/lab host="DH108"
/clone_lib="COGENE 6E MAX"
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Homo sapiens
            sapiens (human)
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Unpublished (1997)
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Matches 124; Conservative
                               Homo sapiens
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AQ109589 451 bp DNA linear GSS 29-AUG-1998 CIT-HSP-2373020.TR CIT-HSP Homo sapiens genomic clone 2373020, genomic survey sequence.
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Map Building
Unpublished (1998)
Other_GSSs: CIT-HSP-2373020.TF
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Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 10449764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="CIT_Approved Human Genomic Sperm Library /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones i B-Coli DH10B"
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                                                                                                                            Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2031 row: K column: 18
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Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=2033 Col=18 Row=K"
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constructed by Bento Soares and M. Fatima Bonaldo.
              /tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 TGCTGGTGTGCTGCACCACTAACTC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 TGCTGGTGTGCTGCACCCATTAACTC 161
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1 (bases 1 to 1577)
Strausberg, R.
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Email: Gapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 614 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 456.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST 01-FEB-1999
              Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 İCİTİTİTIRITİRITIAİTİTATITATITATİTATİTATİTATİTİRİTATİATAC-İ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                  75
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI310239 541 bp mRNA linear EST 01-FEB-19: qo75h12.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1914407 3' similar to contains L1.b1 L1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae, Homo.
1 (bases 1 to 541)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                              16 TITITITITITIGALGALITITAATAAATATCATTITCTITITITITATTATACTT
                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                           /cell type="Sperm"
/clone lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                       Score 100.4; DB 11; Length 451;
Pred. No. 7.8e-08;
0; Mismatches 21; Indels 1;
                                                                                                                                        1. .451
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="taxon:9606"
/clone="2373020"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCTGGTGTGCTGCACCCATTAACTC 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 TGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI310239.1 GI:4005110
                                                                                                                                                                                                                                                                                                                                                         14.3%;
84.9%;
                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 84.9
Matches 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumor Gene Index
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AUTHORS
TITLE
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                                                                                                                       FEATURES
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                                                                                                                                                                                                                                    Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                        75
                                                                                                                                                                            92
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 19 Row: a Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein
                                                                                                                                                                1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: David N. Louis, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
   DB 1; Length 541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone has the following problem: retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                             21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
14.3%; Score 100.4; DB 1, 84.9%; Pred. No. 7.8e-08; iive 0; Mismatches 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1577 bp mRNA
Homo sapiens, clone IMAGE:4150580, mRNA.
BC010517
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RZPD; RZPDB737B122008D; RPI1-16D24;
derived from Pieter J. de Jong library RPCI-11;
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDB737B122008D
RZPDLIB; (Human Genomic Set - RZPD 1.0) RZPD LIB No.737
http://www.rzpd.de/cgi-bin/products/sec.cgi?libNo=737
http://www.rzpd.de/products/genomicset/
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                                                                                                                                      ö
                                                                                                                                                                                                         94 GTGCAAAGTGTGCAGGTTAGTTACATATATACATGTGCCATGCTGGTGTGCTGCACCC 153
                                                                                                                                                                                                                                                                                                   468 GTGCACAATGTGCGTTGTTACATATGTATACATGTGCAAAGTTGGTGCGCGCCC 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CR959536 10-JUN-200 Home Sapiens BAC end sequence of RZPDB737B122008D from genomic library (orig. Pieter J. de Jong library RPCI-11), genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (07-JUN-2005) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 515, D-69120 Heidelberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available from RZPD;
Contact RZPD (customer.service@rzpd.de) for further information.
Clone distribution: http://www.rzpd.de/products/genomicset/
Seq-primer: T7 (TAA-TAC-GAC-TCA-CTA-TAG-GG)
Class: BAC ends.
/note="Vector: pBACe3.6; Site 1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC Library"
                                                                                                                                                                                   34 TITAATAAAATATCATTTTCTTTTTTTTATTATTATTATTAAGGTTTTTAGGGTACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 671)
Schwarz,F., Neubert,P., Schneider,D., Peters,M. and Korn,B.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Inge Arlance/yerownicset/
RZPD Deutsches Arlancenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
121 + 49 30 32639 100
Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RPCI-11"
/note="Vector: pBACe3.6; RPCI-11 Human Male BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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Best Local Similarity 76.4%; Pred. No. 8.3e-08;
Matches 123; Conservative 0; Mismatches 38; Indels 0;
                                                                                         Score 100.2; DB 11; Length 572;
Pred. No. 8.4e-08;
); Mismatches 18; Indels 0;
                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="RZPDB737B122008D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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CR959536.1 GI:66957023
                                                                                            14.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                         Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                     154 ATTAACTCA 162
                                                                                                                                                                                                                                                                                                                                                                                                                  528 ACTAACTCA 536
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                                                                                                                    Similarity
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                                                                                              Query Match
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KEYWORDS
SOURCE
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AUTHORS
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JOURNAL
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CR959536
LOCUS
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1 (bases 1 to 572)

RS Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.

Use of BAC End Sequences for Sequence-Ready Map Building
Upublished (1997)

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 0208

Email: maddams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
RACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search/bac_end_search.html
Seq primer: T7

Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S72 bp DNA linear GSS 08-APR-1999
RPCIII-7016.TV RPCI-11 Homo sapiens genomic clone RPCI-11-7016,
genomic survey sequence.
                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:4150580"
/tissue_type="Brain, glioblastoma with EGFR amplification"
/clone_lib="NCI CGAP_Brn64"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                  76 ITAAGITITIAGGGTACATGTGCAAAGTGTGCAGGTTAGTTACATATATACATGTGCCA 135
                                                                                                                                                                                                                                                                                                                                                                       75
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                             Length 1577;
                                                                                                                                                                                                                                                                                                                        21; Indels
                                                                                                                                                                                                                                                                                DB 6;
                                                                                                                                                                                                                                                                             Score 100.4; DB 6
Pred. No. 7.3e-08;
                                                                                                                                                                                                                                                                                                                          0; Mismatches
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/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1454 TGCTGGTGTGCTGCACCCACTAACTC 1429
                                                 'organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism≃"Homo sapiens"
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/db_xref="GDB:7502655"
/db_xref="taxon:9606"
/clone="RPCI-11-7016"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 TGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .572
    Location/Qualifiers
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 84.9%;
Matches 124; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B72257.1 GI:2711408
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Homo sapiens
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KEYWORDS
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B72257
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AUTHORS
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JOURNAL
COMMENT
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         FEATURES
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Bult.C.J., Lee,N.H., Kirkness,E.F., Weinstock, K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzbugh,W.M., Fitzchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shriey,R., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Ferris,A., Fischer,C., Hastings,G.A., Ho,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Maissner,P.S., Olsen,H., Raymond,L., Weil Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                     AA344409 307 bp mRNA linear EST 21-APR-1997
EST50301 Gall bladder I Homo sapiens CDNA 5' end similar to EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: MIS Reverse
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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/clone_lib="dall bladder!"
/note="Organ: gall bladder!" Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: Xho!"
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1 (bases 1 to 307)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
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14.3%; Score 100; DB 1; Length 307;
Best Local Similarity 80.6%; Pred. No. 9.4e-08;
Matches 129; Conservative 0; Mismatches 30; Indels
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The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
TT: 3108699056
Fax: 3018699423
Email: arkerlav@tigr.org
276 TGTATACATGTGCCATGTGTGTGCTGCACCCACTAACTC 316
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/db_xref="ATCC (inhost):145948"
/db_xref="taxon:9606"
/sex="female"
                                                                                                                                                                                                                                                                                              containing L1 repeat, mRNA sequence.
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/organism="Homo sapiens"
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Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                      AA344409.1 GI:1996648
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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1 (bases I to 870)

Volik, S. V., Raphael, B.J., Huang, G.-Q., Murnane, J., Brebner, J.H.,
Volik, S.V., Raphael, B.J., Huang, G.-Q., Murnane, J., Brebner, J.H.,
Shagin, D.A., Shagina, I.A., Magrane, G., Gray, J.W., Jan, F.-C., de
Jong, P., Pevzner, P. and Collins, C.

Decoding the genomic architecture and high throughput detection of
fusion transcripts in breast cancer cell lines: implications for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS 20-OCT-2005
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                                                                                                                                                                                       /note="Vector: pECBAC1; Site_1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure...
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MCF731m05TF Human MCF7 breast cancer cell line library (MCF7 1)
Homo sapiens genomic clone MCF7_31m05, genomic survey sequence.
2 IGTITCACAIAAAGITITITITITITGAIGATITITAATAAAATAICAITITITITITA
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Best Local Similarity 76.4%; Pred. No. 8.2e-08;
Matches 123; Conservative 0; Mismatches 38; Indels 0;
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UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 SO2 7066
Fax: 415 SO2 565
Email: svolik@cc.ucsf.edu
                                                                                                                                                                                                                                                                                                                                    122 ATATACATGTGCCATGCTGCTGCACCCATTAACTCA 162
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This clone is available from Amplicon Express
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/db_xref="taxon:9606"
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/sex="female"
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Unpublished (2005)
Contact: Volik SV
Colin Collins' lab
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CZ450878
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672 bp DNA linear GSS 20-APR-1999
RPCIIL-53B4.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-53B4,
AQ052012
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Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Vencer, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Unpublished (1998)
Other_GSSS: RPCIII-5384.TK
  GTTAGTTACATATATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTCACATGAA 168
                             375 GTTTGTTACATATGTATACATGTGCCATGTTGGTGTGTGCTGCATCCATTACATTAACTCGT 316
                                                                                                                                                                                           229 ATCCATAAATTTGAAAAAAGTTTAACTACTCTGATAAAAAAGTTTTATAGTTTTCCTACT 288
                                                                                                                                                                                                                                          256 TCTTTCCCAATTCCGGTGTTTCTCAAGTTTTTTAAATTTTTTGTCTTCCACTAATAGATA 197
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                                                                                                                                            315 CATITITIT - TATTATACTITATGCAAATTAAATTAACTGGCAATCCATTTCTTTGCTA 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieters@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (lift@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
class: BAC ends.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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/clone lib="RPC1-11"
/note="Vector: pBAce3.6; Site_1: BcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                      289 ITTAAGCAAAATTCCATAGGGCATGGTAATTGTAGTTTCAACATTACTTGCAGTTTCAGT
                                                                                                169 GTTTTTTTAAATTTTAGTGACAGTTTTAGTCATTTTTCCTAATTGAAAGTATCATAAGTA
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Pred. No. 9e-08;
0; Mismatches 125; Indels
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Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7519995"
/db_xref="texon:9606"
/clone="RRCI-11-5384"
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Best Local Similarity 59.6%;
Matches 186; Conservative
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                   349 TAGTAAATAAAT 360
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    109
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AQ052012
LOCUS
DEFINITION
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It bases 1 to 621)

RS Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Relton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scaarce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marta, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Milliams, T., Jackson, Y. and Bowers, Y. Cole, R., Tsagareishvili, R., Milliams, T., Jackson, Y. and Bowers, Y. Endocrine Pancreas Consortium

AL Upublished (2000)

Other ESTS: isloal2.xl
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
                                                                                                                                                                                                                      is10al2.yl HR85 islet Homo sapiens CDNA clone IMAGE:6364319 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITIATTITIATTITITITATIATACTITITAAGTITIAGGGTACATGTGCACAATGTGCAG 376
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Email: dmetcon@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
asshington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.3%; Score 100; DB 4; Length 621; 59.6%; Pred. No. 9.1e-08; cive 0; Mismatches 125; Indels
                                                                         122 ATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                  121 GTATACATGTGCCATGCTAGTGCTGCTGCACCCATTAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (hinoue@im.wustl.edu)
Seq primer: -dUDF from Gibco
High quality sequence stop: 481.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          CA947015.1 GI:27439892
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
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Fax: 617-495-8557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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Matches 186;
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CA947015/c
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Butaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 272)

2 Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J. C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)

2 Other GSSs: RPCII1-75A2.TJ

Contact: Mark Adams

The Institute for Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                            GSS 27-APR-1999
                                                                                                                                                                                                    Email: mdddms@figr.org
Clones are derived from the human BAC library RPCI-11.. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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/clone_lib="RPC1-11"
/noce="Vector: pBAce3.6; Site_1: EcoR1; Site_2: EcoR1;
RPCII1 Human Male BAC Library"
                                                                                                                 37 idiringriringriririringririringriringriringriringriringririra
                                                                                                                                                             TITITITICATGATTTTAATAAAATATCATTTTCTTTTTTA
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      Pred. No. 9e-08;
0; Mismatches 30; Indels
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                                                                                                                                                                                                                                                                          156 GTATACATGTGCCATGCTGTGCTGCTGCACCCACTAACTC 195
                                                                                                                                                                                                                                                     122 ATATACATGTGCCATGCTGGTGCTGCACCCCATTAACTC 161
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/mol_type="genomic DNA"
/db_xref="GDB:7528417"
                                                                                                                                                                                                                                                                                                                                                                                                         272 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/clone="RPCI-11-75A2"
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1. .272
                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQ266524.1 GI:3794128
      al Similarity 80.6%;
129; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
                                                                       TGTTTCACATAAAGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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    Similarity
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    Best Local
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DKRZp313M126_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
NKSZp313M126_5', mRNA sequence.
TITICITITITIATTATTATACTITITAAGTTTTTAGGGTACATGTGCAAAGTGTGCAG 108
                       168
                                                                                                                 228
                                                                                                                                                                                                                     328 CATITITIT-TATTATACTITIATGCAAATTAAATTTAACTGGCAATCCATTTCTTTGCTA 386
                                                                                                                                                                                                                                                                   229 ATCCATAAATTTGAAAAAATGTTAACTACTCGATAAAAAAGTTTTATAGTTTCCTACT 288
                                                                                                                                                                                                                                                                                                                    446
                                                                                                                                                                                                                                                                                                                                                           289 TITAAGCAAAATICCATAGGCATGGTAATIGTAGTITCAACATTACTTGCAGTITCAGT 348
                                                                                                                                                                                                                                                                                                                                                                                                         506
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1 (bases 1 to 677)
Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKE2); Email s.wiemanndökfz- heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the CDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hlcc2)"
Site_1: SfiIA; Site_2: SfiIB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No sl sequence available.
This clone (DKFZp313M126) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  GTTAGTTACATATATATACATGTGCCATGCTGTGTGCTGCACCCATTAACTCACATGAA
                                                                                                                                                                           169 GTTTTTTTAAATTTTTAGTGACAGTTTTTAGTCATTTTCCTAATTGAAAGTATCATAAGTA
                                                                                                                                                                                                                                                                                                               387 TCTTTCCCAATICCGGTGTTTCCCAAGTTTTTTAAATTTTTGTCTTCCACTAATAGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wiemann, S.
EST (Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., et al.)
Unpublished (2003)
On Aug 10, 2001 this sequence version replaced gi:15165163.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="313 (synonym:
/note="Vector: pTriplEx2;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="DKFZp313M126"
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49
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14.3%; Score 100; DB 1; Length 677;

Query Match

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    .505
    /organism="Homo sapiens"

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Genome Res. 16 (1), 55-65 (2006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
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/clone="FCBBF3017123"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                  DAŠ02536
DAS02536.1 GI:80539325
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Best Local Similarity 77.1%;
Matches 121; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Takao Isogai
                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                             sapiens
                                                     equence.
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B92240
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KEYWORDS
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DA502536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J.,
Hoon, S.T., Chu, M., Kim, H., Joo, S., Kim, C., Song, W. and Yoo, H.
Direct Submitssion

Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
52, Oun-dong, Yusong-gu, Dacjeon 305-333, Korea
(E-mail:redgtone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
Tel:82-42-866-7181, Fax.82-42-860-4409)

Clones are derived from the chimpanzee BAC library RP-43 This BAC
end was generated during the R&D process and may have higher chance
PRIMERS
                                                                                                                                                                             AG189910 352 bp DNA linear GSS 06-MAR-2004
Pan troglodytes DNA, clone: RP43-064003.T7, genomic survey
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Park, H., Kim, Y., Kim, S., Han, Y., Woo, T., Park, K., Eun, C.J., Hoon, S.T., Chu, M., Kin, H., Joo, S., Kim, C., Song, W. and Yoo, H. BAC end sequences of Library RP-43
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="lymphocytes"
/clone_lib="RP-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
14.2%; Score 99.4; DB 14; Length 352;
Best Local Similarity 84.8%; Pred. No. 1.2e-07;
Matches 123; Conservative 0; Mismatches 21; Indels 1;
                                                                      201 ATACATGTGCCATGCTGTGCTGCTGCACCCATTAACTC 238
                                                     124 ATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .352
/organism="Pan troglodytes"
/mol type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-064003.T7"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGTGTGCTGCACCCATTAACTCA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGTGTGCTGCACCCATTAACTCA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                     Pan troglodytes (chimpanzee)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequencing: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 352)
                                                                                                                                                                                                                                                                                                                                                           Hominidae; Pan.
                                                                                                                                                                                                                                    AG189910
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                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                             DEFINITION
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JOURNAL
REFERENCE
                                                                                                                                           RESULT 32
AG189910
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AUTHORS
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JOURNAL
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KEYWORDS
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RESULT 33

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548 bp DNA linear GSS 09-APR-1999
RPCIII-20X18.TPB RPCI-11 Homo sapiens genomic clone RPCI-11-20X18,
B92240
B92240.1 GI:2971351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: flj-cdna@nifty.com
NBDO human CDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
DA502536 DA502536 FCBBF3 Homo sapiens cDNA clone FCBBF3017123 5', mRNA
                                                                                                                                                                                                                                                                    Hominidae, Homo.

I (bases 1 to 505)

Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
Ishi,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
Muraskawa,K., Ishidashi,T., Takahashi-Fujii,A.,
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 99.4; DB 9;
Pred. No. 1.2e-07;
0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue type="brain"
/dev stage="fetal"
/clone_lib="FCBBF3"
/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
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10-661966-1 146001-146700 a146311.rst

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Unpublished (1997)
Contact Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
Contact Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the In.A.G.E. Consortium/LNLL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA
sequence: 2-54, >(TAAA)n#Simple_repeat (matched compliment) 57-287,
Seq primer: M13 FORWARD
POLYA=Yes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_libe_NCC_CGAPEIO.
/clone_libe_NCC_CGAPEIO.
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCL_CGAP_EIO is a cDNA library containing the following
tissue(s): Chondrosarcoma. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT18 tail. The
sequence tag for this library is ACACTTGCAC.
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     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon.9606"
/clone="IMAGE:5838669"
/tissuu-fhondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 99.4; DB 3;
Pred. No. 1.1e-07;
0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAG_TISSUE=chondrosarcoma
TAG_LIB=UI-H-EI0
TAG_SEQ=ACACTTGCAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 TGCTGGTGTGCTGCACCCATTAACT 160
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84.8%;
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Homo sapiens
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Best Local Similarity
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Matches
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BQ924499/c
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     AUTHORS
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                                                                                                          Adams, M. D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Gadams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Use of EAC End Sequences for Sequence-Ready Map Building (1998)

Unpublished (1998)

Other_GSS: RPCIII-20K18.TV

Contact: Mark Adams

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208

Fax: 301 838 0208

Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-II. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
RACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (inf@resgen.com). BAC end search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ007697 171 bp mRNA linear BST 26-MAR-2002 UI-H-EIO-ayh-c-22-0-UI.S1 NCI_CGAP_EIO Homo sapiens cDNA clone INAGE:5838669 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286 TICACALTITITITITITITIAAGIGIGIAACCCCIAGAATITIGITITITITITITI 345
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 TICACATAAAGTITITITITITITIGATGATITITAATAAAATATCATITITITITITATTA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Lymphocytes"
/clone lib="RPC1-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 TACATGTGCCATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .548
/organism="Homo sapiens"
/mol type="genomic DNA"
/db xref="taxon:9606"
/clone="RPCI-11-20K18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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BQ007697.1 GI:19732597
                         sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae, Homo.
1 (bases 1 to 771)
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                                                Homo sapiens
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Matches 121; Conserv
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BQ007697
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Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)

Other GSSs: RPCIII-10717.TJ

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.mec.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305 GTTTTAGGGTACATGTGCACAATGTGCAGTTTGTTACATATGTATACATGTGCCATGCT 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moree,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-warck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA446110

401 bp mRNA linear EST 03-JUN-1
Zw60b03.s1 Soares total fetus NB2HP8-9w Homo sapiens CDNA clone
IMAGE:774413 3' similar to 9b:i19872 AH RECEPTOR PRECURSOR
(HUMAN);contains L1.b2 L1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /ccll type="Lymphocytes"
/clone lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 TITITITIGAIGAITITAATAAAATAICATTITICITITITITITATTATAATACTITIAA
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 GGTGTGCTGCACCCATTAACTCTTTAGCATTAGGTATATCT 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 GGTGTGCTGCACCCATTAACTCACATGAAGTTTTTTTAAATTT 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 99.2; DB 11;
Pred. No. 1.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol type="genomic DNA"
/db xref="GDB:7540902"
/db xref="taxon:9606"
/clone="RPCI-11-10717"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Best Local Similarity 79.3%;
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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ORGANISM
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AUTHORS
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AA446110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="Lupski sciatic nerve"
/note="Vector: pGWV-SPORT6 (Life Technologies); Site_1:
/note="Vector: pGWV-SPORT6" (Life Technologies); Site_1:
Not1; Site_2: Sall; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTATCAGATCGAGGGGCGCCCCT(IS)-3'. Size selected >
1' kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor Technologies and is available through Life
Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  571 bp DNA linear GSS 06-WAY-1999 RPCI1-10717.TV RPCI-11 Homo sapiens genomic clone RPCI-11-10717, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148
                                                                                                                                                                      Email: cgapbe_r@mail.hih.gov
Tissue Procurement: Dr. James R. Lupski
DNN Albrary Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM13608 row: p column: 09
High quality sequence stop: 554.

1. 906

1. 906
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I (bases 1 to S71)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo.

1 (bases 1 to 906)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Pred. No. 1.1e-07;
0; Mismatches 36; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 ACATGTGCCATGCTGGTGTGCTCCACCCATTAACTCA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACATGTGCCATGTTGCTTTGCTGCACCCATTAACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tissue type="sciatic nerve"
/dev stage="adult, 70 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="lYAGE:6198008"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ319769.1 GI:4052657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14.2%;
ilarity 77.1%;
Conservative
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Best Local Similarity
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                                                          REFERENCE
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AQ319769
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AUTHORS
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a 8 g δ g

Gaps

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EST 03-JUN-1997

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Hominidae, Homo.

I (bases 1 to 553)

Kimura, K., Wakamatu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Kimura, K., Wakamatu, A., Sekine, M., Tsuritani, K., Wakaguri, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
Wurakawa, K., Ishida, R., Ishibashi, T., Takahashi Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
Genome Res. 16 (1), 55-65 (2006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 03-DEC-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                         /cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 TTAGGGTACATGTGCACATTGTGCAGGTTAGTTACATATGTATACATGTGCCATGCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTTTGATGATTTTAATAATATCATTTTCTTTTTTTTATTATTATAACTTTAAAGTT
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DB302517 BRAMY2 Homo sapiens cDNA clone BRAMY2030702 3', mRNA
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Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 99; DB 11; Length 46
Pred. No. 1.4e-07;
0; Mismatches 25; Indels
                                                                                                                                                                                                           organism="Homo sapiens"
                                                                                                                                                                                                                                   /mol_type="genomic_DNA"
/db_xref="GDB:7515691"
/db_xref="taxon:9606"
/clone="RPCI-11-41N20"
                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143 GIGCIGCACCCATTAACTC 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB302517.1 GI:83085415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.1%;
82.0%;
                                                                                                                                                                                                                                                                                                                                       /sex="Male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114; Conservative
                                                                                                                                 Class: BAC ends.
                                                                                                                                                                                   1. .464
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                               /clome_lib="Soares_total_fetus_Nb2HF8_9w", hote="Vector: pT773-Pac1; Site_1: Not II, Site_2: Eco RI; lst strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus material with a Not I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ029723 464 bp DNA linear GSS 14-APR-1999
RPCIl1-41N20.TV RPCI-11 Homo sapiens genomic clone RPCI-11-41N20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 464)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and
Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 TITITITICATGATTITIAATAAATATCATTITCTTTTTTTTATTATTATAAC 80
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fax: 314 286 1810
Email: estewastson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. ET from Amersham
High quality sequence stop: 369.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Use of BAC End Sequences for Sequence-Ready Map Building (1998) Unpublished (1998)
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Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 14.1%; Score 99; DB 1; Length 401; Best Local Similarity 86.5%; Pred. No. 1.4e-07; Matches 122; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:774413"
                                                                                                                                                                                                                                                                                                                               /dev_stage="8-9 weeks"
/lab_host="DH108"
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AQ029723
AQ029723.1 GI:3274854
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Homo sapiens
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Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Center, National Institute of Technology and Evaluation; 3'-end one
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                                                                                                                                                                                                                                                                                                                                           79 AGTITITAGGGIACATGTGCAAAGTGTGCAGGTTAGTTACATATATACATGTGCCATGC 138
                                                                                                                                                                                                                                                                                                                                                                                                  AG042325 665 bp DNA linear GSS 01-NOV-2003
Pan troglodytes DNA, clone: PTB-020E21.F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                         78
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                         Gaps
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fuliyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                  14.1%; Score 99; DB 9; Length 553; 85.3%; Pred. No. 1.4e-07; ive 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-020E21.F"
                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db xref="texon:9606"
/clone="BRAMY2030702"
/clone lib="BRAMY2"
/clone lib="BRAMY2"
/note="Vector: pME18SFL3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 TGGTGTGCTGCACCCATTAACTC 161
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               pass sequencing: RAB.
Location/Qualifiers
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 665)
                                                                                                                                                                                                                                                    Best Local Similarity 85.3
Matches 122, Conservative
                                                    1. .553
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AUTHORS
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AG042325
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High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA 701 Queen Anne Avenue North, Seattle, WA 98109, USA 701 Queen Anne Avenue North, Seattle, WA 98109, USA 701 Queen Anne Avenue North, Seattle, WA 98109, USA 701 Gen-Sale Fax: (206) 616-3887

Fax: (206) 616-3887

Email: jwallace@u.washington.edu

Library availability, please contact Pieter de Jong

Library availability, please contact Pieter de Jong

Library availability, please contact Pieter de Jong

Library availability, please contact Pieter de Jong

Location/Gualifiers

Location/Qualifiers
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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1 (bases 1 to 704)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS 02-AUG-1999
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ779743 10 SP6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1147 Col=20 Row=P, genomic survey sequence.
                                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                 Gaps
                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                           Length 665;
                                                                                                                                 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
Mol type="genomic DNA"
/db xref="rexon:9606"
/clone="Plate=1147 Col=20 Row=P"
                                                                           DB 14;
1.4e-07;
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                                                                           14.1%; Score 99; DB
85.3%; Pred. No. 1.4e
:ive 0; Mismatches
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                                                                                                    Best Local Similarity 85.3
Matches 122; Conservative
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Hominidae, Homo.

1 (Dases I to 42)

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Building (1998)
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1 (Dases I to 468)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                  Unpublished (1998)
Other GSSs: CIT-HSP-2328018.TF
Contact: Mark Administration of Bulling and State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of State of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: Ml3 Reverse
Class: BAC ends.
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HS_3094_A1_B02_MF CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3094 Col=3 Row=C, genomic survey
                                                               Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.1%; Score 98.8; DB 11; Length 424; 79.6%; Pred. No. 1.5e-07; tive 0; Mismatches 32; Indels 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="2328018"
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                                     sapiens (human)
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(bases 1 to 419)

Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,

Bevignes, M. D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B.,

Lorenzo, F., Mitchell, H., Mariage-Samson, R., Pietu, G., Poullot, Y.,

Sebastiani Kabaktchis, C. and Tessier, A.

IMAGE: molecular integration of the analysis of the human genome
                                                                                                                                             18 TATTITIATITIATITIATITITICCTATTAACATTITITIATITATIATIATIA 77
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
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Pred. No. 1.4e-07;
0; Mismatches 25; Indels
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Am Klopferspitz 18a,8033 Martinsried,Germany
Email: obermaier@vms.biochem.mpg.de
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89.8%; Pred. No. 1.5e-07;
ative 0; Mismatches 12;
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                                                         Matches 125; Conservative
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E 1 (bases 1 to 561)

S Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building

Dupublished (1997)

Cother GSSs: RPCI-11-383F14.TJ

Cother CSSs: RPCI-11-383F14.TJ

Cother CSSs: RPCI-11-383F14.TJ

Cother CSSs: RPCI-11-860 William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Fat: 301 838 0200

Fax: 301 838 0208

Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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0
                                                                                 Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3094 row: C column: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
14.1%; Score 98.8; DB 11; Length 468;
Best Local Similarity 78.7%; Pred. No. 1.5e-07;
Matches 118; Conservative 0; Mismatches 32; Indels 0
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                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=3094 Col=3 Row=C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215 TGACATGCTGGTGCGCTGCACCACTAACT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 TGCCATGCTGGTGTGCTGCACCCATTAACT 160
                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                   High quality sequence stop: 468.
Location/Qualifiers
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AQ550918.1 GI:4910095
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ORGANISM
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AUTHORS
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COMMENT
                                                                       PUBMED
                                                 JOURNAL
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           TITLE
                                                                                       COMMENT
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Conteact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLONE Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this CDNA
sequence: 1-48, > (TAAA) h#85.mple repeat (matched compliment) 51-169,
>LIPRA#LINE/L1 (matched compliment) 413-454,
>AT Tich#Low complexity 498-590, >MIR#SINE/MIR (matched compliment)
POLYA=Yes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BQ447264 1-23-0-UI.s1 NCI CGAP_Ct1 Homo sapiens CDNA clone
UI-H-EU1-bad-1-23-0-UI.s1 NCI CGAP_Ct1 Homo sapiens cDNA clone
UI-H-EU1-bad-1-23-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    library availability, please contact Pieter de Jong pietersdebing, med. buffalo.edu. Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.seq primer: T7 class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Homoinidae; Homo.

1 (Bases 1 to 725)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="Lymphocytes"
/clone lib="RFCI-11"
/note="Vector: pBACe3.6; Site_1: BcoR1; Site_2: BcoR1;
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 ATACATGTGCCATGCTGGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 98.8; DB 11;
Pred. No. 1.5e-07;
0; Mismatches 37;
                                                                                                                                                                                                            Location/Qualifiers
1. 561
/organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                       /mol_type="genomic_DNA"
/db_xref="GDB:7646821"
/db_xref="taxon:9606"
/clone="RPCI-11-383F14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 76.6%;
Matches 121; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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169

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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland,
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele.K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dietrich,N.L., Granife,S., Guan,X., Gupta,J., Hadpighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,O.L., Massiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                              /note="Vector: pECBACI, Site 1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Homo. (bases 1 to 3088)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                             /clone_lib="Human MCF7 breast cancer cell line library (MCF7 1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 TITITITITITIGATGATITITAATAAATATCATITICTTTTTTTTTATTATTACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 98.8; DB 13;
Pred. No. 1.5e-07;
0; Mismatches 22;
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Homo sapiens, clone IMAGE:5210997, mRNA.
BC032464
                                                                              1. .853
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 TGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 TGCTGGTGCGCTGCACCCATTAAGTC 84
                                                                                                                                 /mol_type="genomic_DNi
/db_xref="taxon:9606"
/clone="MCF7_25h15"
/sex="female"
                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BC032464.1 GI:22749645
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  http://www.genomex.com
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                14.1%;
84.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
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Best Local S
                                                                                   source
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BC032464/c
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ORGANISM
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                                        /clone="UTH-EUI-bad-1-23-0-UI"
/tissue_type="Gatecoarthritic Cartilage"
/de_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/clone lib="NCI CGAP Ct1"
/note="Gorgan: Knee; Vector: pT7T3-pac (Pharmacia) with a modified polylinker; Site 1: EcoR 1; Site 2: Not 1;
NCI CGAP Ct1 is a normalized cDNA library_containing the following tissue(s): Osteoarthritic Cartilage The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ilgated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector: The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CZ446241 GSS 20-OCT-2005 MCF725h15TF Human MCF7 breast cancer cell line library (MCF7_1) Home sapiens genomic clone MCF7_25h15, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae, Homo.

1 (bases 1 to 813)
Volik,S.V., Raphael,B.J., Huang,G.-Q., Murnane,J., Brebner,J.H.,
Bajsarowicz,K., Paris,P., Tao,Q., Kowbel,D., Lapuk,A.V., Kuo,W.-L.,
Shagin,D.A., Shagina,I.A., Magrane,G., Gray,J.W., Jan,F.-C., de
Jong,P., Pevzner,P. and Collins,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Decoding the genomic architecture and high throughput detection of fusion transcripts in breast cancer cell lines: implications for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 rirriririririririrareaGacircrirarirarirarirarirariarirariac-r 60
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 TITITITITITIGALGALTTTTAATAAATATCATTTTCTTTTTTTTTTATTACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (dT)18 tail. The sequence tag for this library is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 725;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAG_TISSUE=osteoarthritic cartilage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 98.8; DB 3
Pred. No. 1.5e-07
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTGGTGTGCTGCACCCATTAACTC 161
                           xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAG_LIB=UI-H-EU1
TAG_SEQ=TGATCACGCT"
'mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CZ446241.1 GI:77922503
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84.2%;
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Unpublished (2005)
Contact: Volik SV
Colin Collins' lab
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Best Local (
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CZ446241/c
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HTC 06-SEP-2002

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Homo sapiens (human)
                                    /sex="Male"
                                                                                                                                                                                                         Matches 117; Conservative
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                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
AQ605001
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VERSION
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COMMENT
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Serieg: IRAK Plate: 64 Row: j Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 bp DNA linear GSS 09-JUN-1998 CIT-HSP-2304Al3.TR CIT-HSP Homo sapiens genomic clone 2304Al3, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                               ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.

1 (bases 1 to 324)

Adams, M.B. 1 to 324)

Adams, M.B. Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.,

Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,

Sinon, M., and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map

Building (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
Other GSSs: CIT-HSP-2304Al3.TF
Contact: Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 818 0208
Email: maddams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                  75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Gaps
                                                                                                                                                                                                                                                                                                                                                        Length 3088;
                                                                                              analysis
This clone has the following problem: frame shifted.
                                                                                                                           Location/Qualifiers
1. 3088
1. 3088
(organism="Nomo sapiens"
/mol type="mRNA"
/db xref="texon:9606"
/clone="IMAGE:5210997"
/tissue type="Blood, adult leukocytes"
/lab host="DHIOB"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                             22; Indels
                                                                                                                                                                                                                                                                                                                                                        Query Match
14.1%; Score 98.8; DB 6;
Best Local Similarity 84.2%; Pred. No. 1.4e-07;
Matches 123; Conservative 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 TGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ĀQ017761
AQ017761.1 GI:3196497
                                                                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AQ017761
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AUTHORS
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COMMENT
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3861
Fax: (206) 616-3861
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2119 row: B column: 23
Seq primer: T7
Class: BAC ends
High quality sequence stop: 398.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae; Homo.

1 (bases 1 to 398)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ605001
HS 2119_B1_A12_T7C CIT Approved Human Genomic Sperm Library D Homo
sapiens Genomic clone Plate=2119 Col=23 Row=B, genomic survey
                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 ACTITIAAGITITIAGGGIACAIGIGCAAAGIGIGCAGGITAGITACATATATATATACATGI 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                    12 AAAGTITITITITITGATGATTITAATAAAATATCATTITCTTTTTTTTATTATTAT
                                                                                                                                                                                                                                                                                                            Gaps
                                                                   /cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                              14.1%; Score 98.4; DB 11; Length 324; 79.1%; Pred. No. 1.8e-07; ive 0; Mismatches 31; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .398
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=2119 Col=23 Row=B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 GCCATGCTGGTGTGCTGCACCCATTAAC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 GCCATGCTGTGCTGTACCCACTAAC 289
/db_xref="taxon:9606"
/clone="2304A13"
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10-661966-1 146001-146700 a146311.rst

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Gaps

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275

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EST 21-FEB-2003

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/organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="Uto-FrNO-aeu-e-07-0-UI"
/lab_host="Human Lung Epithelial cells"
/lab_host="Human Lung Forthelial cells"
/lone="Torgan: Lung: Vector: pT773-pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
/U-CF-FNO is a subtracted CDNA library derived from two normalized Human lung epithelial cell libraries (ENI and DUI) The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems
The following repetitive elements were found in this CDNA sequence: 20-114, >LIPRZ#LINE/L1 (matched compliment) 116-273, >LIBG 5 (matched compliment)
                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae, Homo.
1 (bases 1 to 273)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                             TTTTTTTTTGATGATTTTAATAAAATATCATTTTTTTTT
                                                                                                                                                                                                                                                                                                                                BUG07283
UI-CF-FN0-aeu-e-07-0-UI.S1 UI-CF-FN0 Homo sapiens cDNA clone
UI-CF-FN0-aeu-e-07-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bento-soares@uiowa.edu
TAG TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG_LIB=UI-CF-FN0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Iowa 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 4866 Fax: 319 356 7171 Email: paul-mcray@ujowa.edu Tissue Procurement: Dr. M. J. Welch Interview.
   80.0%; Pred. No. 1.7e-07; ive 0; Mismatches 31; Indels
                                                                                                                                                                                                      121 TATATACATGTGCCATGCTGGTGTGCTGCACCCATTAACT 160
                                                                                                                                                                                                                         335 TGTATACATGTGCCATGCTGGTGTGCTGCACCCATTAAAT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                          BU607283.1 GI:23270558
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                           1 CTGTTTCACATAAAGTT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: McCray, PB
 Best Local Similarity 80.0
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                          RESULT 53
BU607283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
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PUBMED
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                               BX115372 To 713 bp mRNA linear EST 07-FEB-2003 BX115372 Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGP998M18117 ; IMAGE:123065, mRNA sequence.
                                                                                           73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free from RZPD; contact RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                        14 AGTITITITITITATAAAAATAICATITITATAATATAA
                                        Gaps
                                      ;
Score 98.4; DB 11; Length 398;
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGp998M18117 ; IMAGE:123065"
                                        31;
                   Pred. No. 1.8e-07
                                    0; Mismatches
                                                                                                                                                                                                                     134 CATGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                      284 CATGCTGGTGGCTGCACCACTAACTC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .713
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                         BX115372.1 GI:27839389
14.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
               Best Local Similarity /9.1
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                            EST
 Query Match
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DEFINITION
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ORGANISM
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BX115372
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
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14.1%; Score 98.4; DB 4; Length 713;

Query Match

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Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Murakawa, T., Otsuka, R., Randa, K., Yokoi, T., Kondo, H., Wagatsuma, M., Tanase, T., Nagai, S., Ishibashi, T., Takahashi-Fujii, A., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S. Diversification of Transcriptional Modulation: Large-scale Promoters of Human Characterization of Putative Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: fij-cdna@nifty.com
NBDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
                                                                                                                                                                                                                                                         DB097926 DESTI4 Homo sapiens cDNA clone TESTI4049307 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 ATACTITAAGTITTTAGGGTGCATGTGCAATGTGAAGGTTAGTTACATATGTATACATA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378 hriciahigahinghnghgrchranninthrinchrinkhrinahiahiahac-r 436
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 98.2; DB 9;
Pred. No. 1.9e-07;
                                                                                                          161
                                                                                                                                                   201
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14.0%; Score 98.2; D
Best Local Similarity 83.7%; Pred. No. 1.9e
Matches 123; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .560
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pME18SFL3"
                                                                                                                              171 TGCCATGCTGGTGTGCTGCACCCATTAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 TGCTGGTGTGCTGCACCCATTAACTCA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 16 (1), 55-65 (2006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="testis"
/clone_lib="TESTI4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                           sequence.
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                                                                                                          131
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VERSION
                                                                                                                                                                                                                  RESULT 55
DB097926
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COMMENT
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                                                                                                                                                     49 TTTTCTTTTTTTATTATTATTATTATTAAGTTTTAGGGTACATGTGCAAAGTGTGCAG 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhao@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet cs (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

This BAC end was generated during the R&D process and may have

higher chance of clone tracking errors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="Lymphocytes"
/clone_lib="RPC1-11"
/note="Vector: pBACe3.6; Site_1: EcoR1; Site_2: EcoR1;
RPCI11 Human Male BAC Library"
                                                                                                                                                                                Gaps
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae; Homo.
1 (bases 1 to 555)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
                                                                                                                                                                                                                                           109 GITAGITACATATATACATGIGCCATGCTGGTGTGCTGCACCCATTAAC 159
                                                                                                                                                                                                                                                                  64 GITAGTTACCTATGTATACATGTGCCATGCTGGTGCTGCTCCCACTAAC 114
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                                                             Score 98.2; DB 3; Length 273;
Pred. No. 2e-07;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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11arity 78.1%; Pred. No. 1.9e-07;
Conservative 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAC end sequences of library RPCI-11
Unpublished (1997)
Other_GSSs: RPCI-11-357P22.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .555
/organism="Homo sapiens"
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/db_xref="GDB:7637085"
/db_xref="taxon:9606"
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/clone="RPCI-11-357P22"
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TAG_SEQ=GGCTGTAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ519511.1 GI:10831088
                                                               14.0%;
92.8%;
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                                                                                   Best Local Similarity 92.8
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: SP6
Class: BAC ends.
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les 118; Conserv
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                                                                   Query Match
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Matches
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AUTHORS
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AZ519511
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BQ352132 LOCUS DEFINITION

RESULT 56

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ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS JOURNAL PUBMED

COMMENT

TITLE

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Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                          Map Building
Unpublished (1997)
Other GSSs: CITBL-E1-2650L21.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0200
Fax: 301 838 0200
Email: hbe@rigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                        Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBeloBAC11; Site_1: BcoR1; Site_2: EcoR1; CalTech Human BAC Library D"
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 740)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CR958489 17-JUN-20 AND The Linear GSS 07-JUN-20 Homo sapiens PAC end sequence of RZPDB737G0315D from genomic library (orig. Pieter J. de Jong library RPCI-3), genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.0%; Score 98; DB 11; Length 480; 82.7%; Pred. No. 2.1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic_DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="sperm"
/clone_lib="CITBI-E1"
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1. .480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="2650L21"
       survey sequence
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                            AQ628311
AQ628311.1 GI:5090703
                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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1 (bases 1 to 480)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                               Hominidae, Homo.

1 (bases 1 to 226)

1 (bases 1 to 226)

1 (bases 1 to 226)

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.luds.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-HT0619-100700-208-A10&t3=2000-07-10&t4=1)
Seq primer: puc 18 forward High quality sequence stop: 226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: head neck, Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                           8Q352132 220-MAY-2002
IL3-HT0619-100700-208-A10 HT0619 Homo sapiens CDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shorgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.0%; Score 98; DB 3; Length 226; 91.2%; Pred. No. 2.2e-07; tive 0; Mismatches 10; Indels
497 TGCTGGTGTGCTGCACCCATTAACTCA 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="HT0619"
                                                                                                                                                                                               BQ352132.1 GI:21016188
                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 104; Conservative
                                                                                                                                                                                                                                                                              Homo sapiens
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FEATURES

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1; Gaps

GSS 07-JUN-2005

RESULT 57
AQ628311
LOCUS
DEFINITION

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9712 Medical Cente
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 128; Conservative
                                                                                                                                                                                                                         Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pongo
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CR750736/c
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JOURNAL
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1 (bases 1 to 385)

Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and
Venter, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building
Unpublished (1997)
Other GSSs: RPCII1-12116.TV
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                   Action Action Pleter J. Action Library RPCI-3;
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPDB737G0315D
RZPDIJE; (Human Genomic Set - RZPD 1.0) RZPD LIB NO.737
http://www.rzpd.de/cgi-bin/products/set.cgi7libNo=737
http://www.rzpd.de/products/genomicset/
contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Fax: +49 30 32639 100
www.rzpd.de
www.rzpd.de
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                           Submitted (07-JUN-2005) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 515, D-69120 Heidelberg,
                                                                                                                                                                                                                                                                                                                                    This clone is available from RZPD;

Contact RZPD (customer.service@rzpd.de) for further information.

Clone distribution: http://www.rzpd.de/products/genomicset/
Seq-primer: T7 (TAA-TAC-GAC-TCA-CTA-TAG-GG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clōne="RZPDB737G0315D"
/eac="Male"
/clone lib="RPCI-3"
/note="Vector: pCYPAC2; RPCI-3 Human Male PAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 TITCACAIAAAGITITITITITITIGAIGAITITIAAIAAAAIAICAITITITITITITITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Schwarz,F., Neubert,P., Schneider,D., Peters,M. and Korn,B.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 14; Length 740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 14.0%; Score 98; DB 14; Length 74 Local Similarity 80.4%; Pred. No. 2e-07; les 127; Conservative 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       410 ATACATGTGCATGCTGTGTGTGCTGCACTCATTAACTC 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 ATACATGTGCCATGCTGGTGTGCTGCACCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic_DNA"
/db_xref="taxon:9606"
                                                                                                      RZPD; ŘZPDB737G0315D; RP3-416J7;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .740
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                                                                                      Germany
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B75832
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657 bp mRNA linear EST 30-AUG-2004
DKFZp470L1122_r1 470 (synonym: pliv1) Pongo pygmaeus cDNA clone
DKFZp470L1122_5', mRNA sequence.
CR750736
EST.
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This is the 5' sequence of the clone insert Clone from S. Wiemann,
Molecular Genome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz.heidelberg.de, any. Please contact RZPD for
                                                                           Email: maddams@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
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Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hominidae; Pongo.
1 (bases 1 to 65.7)
Poustka, Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R.,
Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pongo pygmaeus mRNA (Poustka,A., Albert,R., Moosmayer,P., et al.)
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukāryotā, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="Lymphocytes"
/clone_lib="RPC1-11"
/note="Vector: pBACe3.6; Site_l: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 TITCACATAAAGITITITITITITIGAIGATITITAATAAAATAICATITITITITITITITITIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           292 ATACATGTGCCGTGCTGCTGCTGCACCCATTAACTCAGA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 ATACATGTGCCATGCTGGTGTGCTGCACCCATTAACTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.0%; Score 97.8; DB 11; 79.5%; Pred. No. 2.3e-07; iive 0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                          1. .385
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic_DNA"
/db_xref="GDB:7504431"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="RPCI-11-12116"
                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex="Male"
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23-APR-1999

468

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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
7e1: (206) 616-3861
Fax: (206) 616-3861
Email: jwallac@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Seq primer: 680 row: B column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae, Homo.
1 (bases 1 to 513)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib-"RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
  349 AAAGTTTTCCCACTATTATTAATTATTTACATAATATTTTTTAATTNTATTATTATTA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                        72 ACTITIAAGTITIAGGGIACAIGIGCAAAGTGIGCAGGIIAGIIACAIAIAIAIAIACAIGI
                                                             409 TACTTTAAAGTTTTAGAGTACAIGTGCACAATGTGCAGGTTTGNTACATAGTATACATAGTA
                                                                                                                                                                                                                                                               AQ464599 linear GSS 23-APR-HS_5104 BZ_A11_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=680 Col=22 Row=B, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTTTTTTTTGATGATTTTAATAAAATATCATTTTCTTTTTTTATTATTATACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.9%; Score 97.6; DB 11; Length 513; 79.9%; Pred. No. 2.4e-07; ive 0; Mismatches 29; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=680 Col=22 Row=B"
                                                                                                                                         469 GCCATGTTGGTGTGCTGCACCCATCAACTCA 499
                                                                                                                   132 GCCATGCTGGTGTGCTGCACCCATTAACTCA 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .513
/organism="Homo sapiens"
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High quality sequence stop: 513.
Location/Qualifiers
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AQ464599.1 GI:4641694
                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Matches
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SOURCE
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                                                                                        /tissue_type="liver"
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="470 (synonym: pliv1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
                                                                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                                                                        136
                                                                                                                                                                                                                                                                                                                          92
                                                                                                                                                                                                                                                                                                                                                                                                                                              41
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                   TITITITITITGATGATITITAATAAATATCATTITITITITITITATTATATACTTT
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call_type="ptimary marginal zone B-cell lymphoma"
/clone lib="Homo sapiens skin ALU-PCR"
/note="ALU-PCR fragment obtained with ALU4 primer"
                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                          Length 657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae, Homo.

1 (bases 1 to 724)
Bertoni,F., Willenbach,R., Broggini,M., Roggero,E.,
Cotter,F.E. and Zucca,E.
Extranodal marginal zone B-cell lymphoma genotyping
                                                                                                                                                                                                                                       Score 97.8; DB 8; Length 6
Pred. No. 2.2e-07;
0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dept. of Oncology
Istituto di Ricerche Farmacologiche 'Mario Negri'
via Eritrea 62, Milan, 20157, Italy
absent in matched peripheral blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alu-polymerase chain reaction
Leuk. Lymphoma 38 (5-6), 605-610 (2000)
10953982
                  /organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
                                                                              clone="DKFZp470L1122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 GCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DN;
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: Alu-PCR.
Location/Qualifiers
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                                                                                                                                                                                                                                          14.0%;
84.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Bertoni F
                                                                                                                                                                                                                                                          Best Local Similarity 84.1
Matches 122; Conservative
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Matches 117; Conserv
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source
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SOURCE
ORGANISM
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AF118407
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Query Match
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JOURNAL
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AUTHORS
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                                                                                                                                                                          CZ465237 108 bp DNA linear GSS 20-OCT-2005 MCF756k05TF Human MCF7 breast cancer cell line library (MCF7_1) Homo sapiens genomic clone MCF7_56k05, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                Hominidae, Homo.

1 (bases 1 to 708)

Volik,S.V., Raphael,B.J., Huang,G.-Q., Murnane,J., Brebner,J.H.,
Bajsarowicz,K., Paris,P., Tao,Q., Kowbel,D., Lapuk,A.V., Kuo,W.-L.,
Shagin,D.A., Shagina,I.A., Magrane,G., Gray,J.W., Jan,F.-C., de
Jong,P., Pevzner,P. and Collins,C.
Decoding the genomic architecture and high throughput detection of
fusion transcripts in breast cancer cell lines: implications for a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pECBACI; Site 1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136 Arcaacritaritciaritritaritritaritritaritritaritritaritraritraritari 195
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor genome project
Unpublished (2005)
Contact: Volik SV
Colin Collins' lab
UCSF Comprehensive Cancer Center
Tel: 415 502 7066
Fax: 415 502 5665
Email: svolik@cc.ucsf.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.9%; Score 97.6; DB 13; 77.6%; Pred. No. 2.4e-07; ive 0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 GTGCCATGCTGGTGCGCTGCACCCACTAACTC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 GIGCCATGCTGGTGTGCTGCACCCATTAACTC 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="MCF7_56k05"
/sex="female"
                                                                          254 TGCTGGTGTGCTGCACCTAAC 277
                                                    136 TGCTGGTGTGCTGCACCCATTAAC 159
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                                                                                                                                                                                                                                                 CZ465237.1 GI:77948426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.genomex.com
Class: BAC ends.
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Homo sapiens
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tes 118; Conserva
                                                                                                                                                                                                                                   CZ465237
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Matches
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AUTHORS
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COMMENT
                                                                                                                                          RESULT 63
CZ465237
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KEYWORDS
SOURCE
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RESULT

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E 1 (bases 1 to 443)

S Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and
Venter, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building
Unpublished (1997)

C ther GSSs: RPCIII-7E20.TP
CONTACT: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA linear GSS 04-NOV-2001 Fan troglodytes DNA, clone: PTB-130G10.F, genomic survey sequence. AG121371
RPCI11-7E20.TV RPCI-11 Home sapiens genomic clone RPCI-11-7E20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="Lymphocytes"
/clone lib="RPC1-11"
/note="Vector: pBAce3.6; Site_1: EcoR1; Site_2: EcoR1;
RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   136 TGCTGGTGTGCTGCACCCATTAACTCA 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
/db_xref="GDB:7502419"
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/clone="RPCI-11-7E20"
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GSS.
Pan troglodytes (chimpanzee)
                                                        genomic survey sequence.
                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Male"
                                                                                                      B72013.1 GI:2711234
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Matches 116; Conservative
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                                                                                                                                                                                Homo sapiens
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ACCESSION
VERSION
KEYWORDS
SOURCE
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Carter, J., Cordes, M., Harris, A., Isak, A., van Brunt, A., Nguyen, C., Du, F., Courtney, L., Kalicki, J., Ozersky, P., Abbott, S., Armstrong, J., Belter, E.A., Caruso, L., Cedroni, M., Cotton, M., Davidson, T., Desai, A., Elliott, G., Erb, T., Fronick, C., Gaige, T., Haakenson, W., Haglund, K., Holmes, A., Harkins, R., Kim, K., Kruchowski, S.S., Strong, C.M., Grewal, N., Goyea, E., Hou, S., Levy, A., Martinka, S., Mead, K., McLellan, M.D., Meyer, R., Randall-Maher, J., Tomlinson, C., Dauphin-Kohlberg, S. et al.
Generation and annotation of the DNA sequences of human chromosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               End-sequence profiling: Sequence-based analysis of aberrant genomes Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003) 12788976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BZ610242 125 bp DNA linear GSS 08-JUN-2003 WHADR41TF Human MCF7 breast cancer cell line library (MCF7_1) Homo sapiens genomic clone MCF7_1-23G10, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 TITAAGITITTAGGGTACAIGIGCAAAGIGIGCAGGITAGITACAIATATATATAGGCC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
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I (bases 1 to 725)

Vollk, S., Zhao, S., Chin, K., Brebner, J.H., Herndon, D.R., Tao, Q., Kowbel, D., Huang, G., Lapuk, A., Kuo, W.-L., Magrane, G., de Jong, P., Gray, J.W. and Collins, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 13.9%; Score 97.4; DB 13; Length 712; Best Local Similarity 78.9%; Pred. No. 2.6e-07; Matches 116; Conservative 0; Mismatches 31; Indels 0
                                                                                                                                                                                                                                                                                                                                                                   63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Chimpanzee genomic DNA"
                                                                                                                                                                                                                                                                                                                   Genome Sequencing Center
Washington University School of Medicine
4444 Forest Park Parkway, St. Louis, MO (
Tel: (314)286-1839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: submissions@watson.wustl.edu
Class: PCR with specific primers.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 434 (7034), 724-731 (2005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic_DNA"
/db_xref="taxon:9598"
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                                                                                                                                                                                                                                                                      15815621
Contact: Joanne Nelson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                              Fax: (314)286-1810
Email: submissions@
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BZ610242
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                                                                                                                                                                                                                            Lobell Lobell, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submitssion
Submitted (102-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
17-22 Suebhiro-chou, Tsurumi, Eu, Yockohama, Kanagawa 230-0045, Japan (E-mail: chimpbes9ac: riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CZ179389 712 bp DNA linear GSS 31-JAN-2005
AC105347Chiol_tc100.bl Chimpanzee genomic DNA Pan troglodytes
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Pan troglodytes
Pan troglodytes
Pan troglodytes
Pan troglodytes
Ban troglodytes
Mamania; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Pan.
I bases 1 to 712)
Hillier,L.W., Graves,T.A., Fulton,R.S., Fulton,L.A., Pepin,K.H.,
Minx,P., Wagner-McPherson,C., Layman,D., Wylie,K., Sekhon,M.,
Becker,M.C., Fewell,G.A., Delehaunty,K.D., Miner,T.L., Nash,W.E.,
Kremitzki,C., Oddy,L., Du,H., Sun,H., Bradshaw-Cordum,H., Ali,J.,
                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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Pred. No. 2.6e-07;
0; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Pan troglodytes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic, genomic survey sequence.
C2179389
C2179389.1 GI:58347682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/clone="PTB-130G10.F"
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R.Site 1 : SacI
R.Site 2 : SacI.
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78.9%;
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                                                                                                                                                                                                                  (bases 1 to 661)
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Matches 116; Conservative
  troglodytes
                                                                      Hominidae; Pan.
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Gaps

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238 bp mRNA linear EST 22-JAN-2001
BM3-NN1203-151100-001-d08 NN1203 Homo sapiens CDNA, mRNA sequence.
BF954789.1 GI:12372064
BST.
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagal,M.A., da Sllva,W. Jr., Zago,M.A., Bordin,S., Costa.F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpsonoundwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM3&t2=PM3-NN1203-151100-001-d08&t5=2000-11-15&t=1)
Seq primer: puc 18 forward
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                              549 GGTACATGTGCACAATGTGCAGGTTAGTTACATATGTATAAATGTGCCATGCTGGTGCGC
                                                                                                            Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
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                               Length 995;
                                                                       16; Indels
                                 DB 6;
                               Score 97.4; DB 6;
Pred. No. 2.5e-07;
0; Mismatches 16
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Location/Qualifiers
                             13.9%;
Best Local Similarity 87.4%;
Matches 118; Conservative C
                                                                                                                                                                                                                                                              147 TGCACCCATTAACTC 161
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BF954789/c
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVNY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
16t strand cDNA was primed with a NotI-oligo(dI) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMvSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CR597534 995 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DG007YE23 of B cells (Ramos cell line) of
                                                                                                                                                                                                     /note="Vector: pECBAC1; Site_1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                        /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="WCF7 1-23G10"
/sex=female"
/clone lib="Human MCF7 breast cancer cell line library
(WCF7_1)"
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                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                           ۲;
                                                                                                                                                                                                                                                                                                                      Length 725;
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1 (Dases I to 995)
Li W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                    13.9%; Score 97.4; DB 12;
84.6%; Pred. No. 2.6e-07;
ive 0; Mismatches 21;
                                                                         'organism="Homo sapiens"
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1. .725
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http://www.genomex.com
Class: BAC ends.
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CR597534
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Homo sapiens (human)
                                                                                                                                                                                                                                                                procedure."
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es 121; Conserv
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67 CTTTAAGTTTTAGGGTACATGTGCACAATGTGCAGGTTTGTTACATATGTATACATGTGC 126
                                                134 CATGCTGGTGTGCTGCACCCATTAACTC 161
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                                                                                                                                     completed: July 19, 2006, 09:20:55
ne : 4416 secs
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation University Genome Sequencing Center Association of Sequencing by: Washington University Genome Sequencing Center Association: NCI-CGAP clone distribution information can be found through the I.M.A.G. E. Consortium/LLNL at:
Www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 379 Std Error: 0.00
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                                                                                                        187 Tririririririririririririririririri 128
                                                                                                                                              /tissue type="poorly differentiated adenocarcinoma with signet ring cell features" hab host="DHIOB" / Tab host="DHIOB" / Tab host="DHIOB" / CAP Gas4" / Note="Organ: Stomach; Vector: pCMV-SPORT6; Site 1: Sall; Stre 2: Notl; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"
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                                                                    75
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hominidae; Homo.

1 (bases 1 to 256)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Umpublished (1997)
                                                                Gaps
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Pred. No. 3e-07;
0; Mismatches 23; Indels 2
    Pred. No. 3e-07;
0; Mismatches 23; Indels
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                                                                                                                                                                                                                                    136 TGCTGGTGTGCTGCACCCATTAACTC 161
                                                                                                                                                                                                                                                          68 GGCTGGTGCTGCACCCACTAACTC 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2184133"
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